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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:19 ; Search time 60 Seconds

(without alignments)
1648.194 Million cell updates/sec

Title: US-09-721-341-2

Sequence: 1819
1 MAFQNSDYDYENENNG.....VEEPFDSGPTPEFTSF1 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	AAW93169 Human HPI
2	1819	100.0	350	2	AAW93169 Human HPI
3	1819	100.0	350	2	AAW93169 Human HPI
4	1819	100.0	350	2	AAW93169 Human HPI
5	1819	100.0	350	2	AAW93169 Human HPI
6	1819	100.0	350	2	AAW93169 Human HPI
7	1819	100.0	350	2	AAW93169 Human HPI
8	1819	100.0	350	2	AAW93169 Human HPI
9	1819	100.0	350	2	AAW93169 Human HPI
10	1819	100.0	350	2	AAW93169 Human HPI
11	1819	100.0	350	2	AAW93169 Human HPI
12	1819	100.0	350	2	AAW93169 Human HPI
13	1819	100.0	350	2	AAW93169 Human HPI
14	1819	100.0	350	2	AAW93169 Human HPI
15	1819	100.0	350	2	AAW93169 Human HPI
16	1819	100.0	350	2	AAW93169 Human HPI
17	1819	100.0	350	2	AAW93169 Human HPI
18	1819	100.0	350	2	AAW93169 Human HPI
19	1819	100.0	350	2	AAW93169 Human HPI
20	1819	100.0	350	2	AAW93169 Human HPI
21	1819	100.0	350	2	AAW93169 Human HPI
22	1819	100.0	350	2	AAW93169 Human HPI
23	1819	100.0	350	2	AAW93169 Human HPI
24	1819	100.0	350	2	AAW93169 Human HPI
25	1819	100.0	350	2	AAW93169 Human HPI

26	862	47.4	164	4	AAW79310 Human p10
27	824	45.3	159	3	AAW41786 Human ORF
28	761	41.8	175	4	AAU18115 Novel hum
29	761	41.8	175	4	AAU18669 Renal and
30	761	41.8	175	4	AAU21655 Novel hum
31	761	41.8	175	4	AAW99976 Human exp
32	761	41.8	175	4	ABD10276 Human cDN
33	761	41.8	175	4	AAU87280 Novel cen
34	761	41.8	175	4	AAU18361 Human end
35	761	41.8	175	5	ABJ05742 Novel hum
36	761	41.8	175	5	ABP6863 Human pol
37	761	41.8	175	6	ABU97284 Human pol
38	761	41.8	175	7	ADC6296 Human neo
39	689	36.2	358	2	AAW3745 Partial s
40	659	36.2	358	2	AAW21689 Human 7TM
41	659	36.2	358	5	AAU1231 Human 7 t
42	659	36.2	378	2	AAW48724 Human V31
43	659	36.2	378	3	AAW21688 Human 7TM
44	659	36.2	378	4	AAW80114 Human CCR
45	659	36.2	378	4	AAW50859 Human CCR

ALIGNMENTS

RESULT 1

AAW93169 standard; protein; 350 AA.

AAW93169;

24-MAY-1999 (first entry)

Human HPIA041 protein.

HPIA041; G-coupled receptor; disease susceptibility; diagnosis; immunise; treatment; FIA041 protein; gene therapy; immune response; vaccine; HIV-2; inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypertension; hypertension; urinary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; benign prostatic hypertrophy; psychotic disorder; neurological disorder; anxiety; manic depression; delirium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; linkage analysis; gene mapping; human.

Homo sapiens.

EP99332-A2.

03-MAR-1999.

17-FEB-1998; 98EP-00301170.

15-AUG-1997; 97US-0055895P.

27-OCT-1997; 97US-00862822.

(SMIK) SMITHKLINE BEECHAM CORP.

Ellis CE;

WPI; 1999-144803/13.

N-PSDB; AAX22557.

New G-coupled receptor (HPIA041) polypeptide and polynucleotide - useful

as diagnostic reagents and for prevention and treatment of cancer, HIV

infections and Parkinson's disease.

Claim 1; Page 22-23; 27pp; English.

This sequence represents a G-coupled receptor, HPIA041 which is useful

for diagnosing susceptibility to diseases by detecting mutations in the

HPIA041 gene, and can diagnose diseases associated with HPIA041 protein

imbalance by determining HPIA041 polypeptide expression levels. Agonists and antagonists of the protein can be used in treatment to activate (agonist) or inhibit (antagonist) HPIA041 activity, in addition to direct administration of antitense sequences to prevent expression, or HPIA041 polynucleotides to treat conditions associated with a lack of HPIA041 protein. Gene therapy may also be used to affect endogenous HPIA041 polypeptide expression. HPIA041 antibodies are useful for inducing an immune response to immunize and prevent disease, and for isolating HPIA041 clones or purifying the polypeptides by affinity chromatography. HPIA041 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented and treated include bacterial, fungal, protozoan and viral infections, particularly HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcers; asthma; allergies; benign prostatic hypertrophy; and psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or Gilles de la Tourette's syndrome. The HPIA041 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis

Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENGTVDYSQYELICIKEDVREFAKFLVFLITVIVIGLAGNS 60
Db 1 MALEQNSTDYEEENENGTVDYSQYELICIKEDVREFAKFLVFLITVIVIGLAGNS 60
QY 61 MVAATAYKKKRTKTDVYIINLAVALDLLFTLPFAVNAVHGWLVGKIMCKITSALT 120
Db 61 MVAATAYKKKRTKTDVYIINLAVALDLLFTLPFAVNAVHGWLVGKIMCKITSALT 120
QY 121 INFVSGMQLACISIDRYAVAVTKVPSQSGVGKPCWIIICVWMAAILLSIPOLVFTYND 180
Db 121 INFVSGMQLACISIDRYAVAVTKVPSQSGVGKPCWIIICVWMAAILLSIPOLVFTYND 180
QY 181 NARCIPFPRIYGTSMKALIQMLEICIGFVFPFLMGVCFITARTLMKMPNIKISRPK 240
Db 181 NARCIPFPRIYGTSMKALIQMLEICIGFVFPFLMGVCFITARTLMKMPNIKISRPK 240
QY 241 VLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMIDIAIQVESIALFHSCLNP 300
Db 241 VLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMIDIAIQVESIALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTFSI 350
Db 301 ILVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 2
AA17435
ID AAY17435 standard; protein; 350 AA.

XX AAY17435;

XX 29-JUL-1999 (first entry)

XX Human signal peptide-containing protein SP-16.

XX Human signal peptide-containing protein; SP; cell proliferation; cancer;

XX neuronal disorder; immune response; detection.

XX Homo sapiens.

XX WO9924463-A2.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US023578.

XX 07-NOV-1997; 97US-00966316.
XX (INCYTE) INCYTE PHARM INC.
XX Lal P, Au-Young J, Reddy R, Murty LB, Mathur P,
XX WPI; 1999-337694/28.
XX DR N-PSDB; AAX61288.
XX CDNA clones encoding signal peptide-containing proteins.
XX Claim 1, Fig 1; 8pp; English.
XX The present sequence represents a human signal peptide-containing protein (SP), designated SP-16. SP proteins can be used to stimulate cell proliferation or to treat or prevent cancer. SP antagonists are also used to treat or prevent cancer, and also for treating or preventing neuronal disorders or immune responses. Polynucleotide sequences complementary to the SP-encoding polynucleotides are useful for the detection of SP-encoding nucleic acid molecules in biological samples

Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENGTVDYSQYELICIKEDVREFAKFLVFLITVIVIGLAGNS 60
Db 1 MALEQNSTDYEEENENGTVDYSQYELICIKEDVREFAKFLVFLITVIVIGLAGNS 60
QY 61 MVAATAYKKKRTKTDVYIINLAVALDLLFTLPFAVNAVHGWLVGKIMCKITSALT 120
Db 61 MVAATAYKKKRTKTDVYIINLAVALDLLFTLPFAVNAVHGWLVGKIMCKITSALT 120
QY 121 INFVSGMQLACISIDRYAVAVTKVPSQSGVGKPCWIIICVWMAAILLSIPOLVFTYND 180
Db 121 INFVSGMQLACISIDRYAVAVTKVPSQSGVGKPCWIIICVWMAAILLSIPOLVFTYND 180
QY 181 NARCIPFPRIYGTSMKALIQMLEICIGFVFPFLMGVCFITARTLMKMPNIKISRPK 240
Db 181 NARCIPFPRIYGTSMKALIQMLEICIGFVFPFLMGVCFITARTLMKMPNIKISRPK 240
QY 241 VLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMIDIAIQVESIALFHSCLNP 300
Db 241 VLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMIDIAIQVESIALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTFSI 350
Db 301 ILVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 3
AAY57290
ID AAY57290 standard; protein; 350 AA.

XX AAY57290;

XX 05-JUN-2000 (first entry)

XX Human BGCKr protein.

XX BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;

XX cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;

XX anti-allergic; antiviral.

XX Homo sapiens.

XX WO9952945-A2.

XX 21-OCT-1999.

PF 16-APR-1999; 99WO-US008395.
XX 16-APR-1998; 98US-00061753.
PR 16-APR-1999; 99US-00061753.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
PI Gonzalo UA, Gutierrez-Ramos JC;
XX WPI; 1999-620375/53.
XX N-PSDB; AA290528.
PT New nucleic acid encoding human BGCKr receptor, used e.g. for modulating
PT inflammation and tumor growth.
XX
XX Claim 8; Fig 2A-B; 123pp; English.
XX
XX The invention relates to a human BGCKr protein, a G-protein coupled
XX receptor. The BGCKr protein can be expressed by standard recombinant
XX methodology. BGCKr are receptor proteins possibly involved in modulation
XX of proinflammatory or stimulatory functions of chemokines; cell
XX proliferation, migration, adhesion and targeting, and exocytosis. The
XX BGCKr nucleic acids and derived proteins (or their variants), antibodies
XX and modulators are potentially useful for modulating inflammation;
XX chemottractant activity of leucocytes; angiogenesis; cell proliferation;
XX tumour growth; allergic reactions and entry of human immune deficiency
XX virus into cells, for therapeutic or prophylactic purposes. They are also
XX used for diagnosis and in drug-screening assays. The present sequence
XX represents the full-length human BGCKr protein
SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYIYENEMNGTVDYSQYELICIKEDVREFAKVLPVLLTIVFVIGLAGNS 60
DB 1 MLEQNSTDYIYENEMNGTVDYSQYELICIKEDVREFAKVLPVLLTIVFVIGLAGNS 60
QY 61 MVAIYAYKKQRTKTDVYIINLAVALDLLFTLPFMAVNAVHGVIGKIMCKITSALYT 120
DB 61 MVAIYAYKKQRTKTDVYIINLAVALDLLFTLPFMAVNAVHGVIGKIMCKITSALYT 120
QY 121 LNFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAILLSTIQVLYTTND 180
DB 121 LNFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAILLSTIQVLYTTND 180
QY 181 NARCIPIPRVYGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLTKMPRIKISRLK 240
DB 181 NARCIPIPRVYGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLTKMPRIKISRLK 240
QY 241 VLLTVVIVFIVTQLPYNIYKFCRAIDITSLTSCMSGRMDIAQVBSIALFHSCLNP 300
DB 241 VLLTVVIVFIVTQLPYNIYKFCRAIDITSLTSCMSGRMDIAQVBSIALFHSCLNP 300
QY 301 ILYVFEGAFKQYVMVAKKYGSWRQROSVVEFPDSEGTPEPTSTFSI 350
DB 301 ILYVFEGAFKQYVMVAKKYGSWRQROSVVEFPDSEGTPEPTSTFSI 350

RESULT 4
AA94325
ID AA94325 standard; protein; 350 AA.
XX
XX AA94325;
XX
XX 11-AUG-2000 (first entry)
XX
XX Human seven transmembrane receptor VSHK-1.
XX
XX Human; seven transmembrane receptor; VSHK-1; signal transduction.
XX

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 6..8
FT Modified-site /note= "potential N-glycosylation site"
FT Modified-site /note= "potential N-glycosylation site"
FT Domain 42..66
FT Domain /label= Transmembrane_domain
FT Domain 79..100
FT Domain /label= Transmembrane_domain
FT Domain 114..135
FT Domain /label= Transmembrane_domain
FT Domain 156..175
FT Domain /label= Transmembrane_domain
FT Domain 199..221
FT Domain /label= Transmembrane_domain
FT Domain 241..262
FT Domain /label= Transmembrane_domain
FT Modified-site 276..278
FT Modified-site /note= "potential N-glycosylation site"
FT Domain 287..308
FT Domain /label= Transmembrane_domain
XX
XX W0200026369-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US025848.
XX
XX 04-NOV-1998; 98US-0107112P.
XX 06-JAN-1999; 99US-0114856P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Khoja H, Shymala V;
XX
XX WPI; 2000-365618/31.
XX N-PSDB; AA94325.
XX
XX Novel polypeptide comprising a new seven-transmembrane receptor protein
XX and its encoding polynucleotide, useful for the analysis of VSHK-1.
XX
XX Claim 3; Fig 1; 79pp; English.

XX The present sequence is VSHK-1, a new seven transmembrane receptor which
XX contains seven membrane-spanning helical domains that are linked by three
XX intracellular and three extracellular loops. The gene sequence encoding
XX VSHK-1 was isolated from a cDNA library. In heart tissue, where VSHK-1 is
XX predominantly found, three RNA species were identified: a 1.3kb, a 2.0kb,
XX and a 5.0kb species. The polynucleotide encoding the present sequence
XX corresponds to the 2.0kb form. The 1.3kb form may result from the use of
XX an alternative polyadenylation site while transcription of a 3.0kb intron
XX at nucleotide 74 could account for the 5.0kb species. VSHK-1
XX polynucleotides can be used as hybridisation probes to detect and measure
XX VSHK-1 mRNA. They may also be used to identify substances that modulate
XX the level of VSHK-1 mRNA. The VSHK-1 coding sequence can be integrated
XX into an expression vector for production of VSHK-1 receptor polypeptides
XX in host cells. The polypeptides can be used to identify agents which
XX modulate VSHK-1 receptor signal transduction activity
XX
XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 3; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLEQNSTDYIYENEMNGTVDYSQYELICIKEDVREFAKVLPVLLTIVFVIGLAGNS 60
DB 1 MLEQNSTDYIYENEMNGTVDYSQYELICIKEDVREFAKVLPVLLTIVFVIGLAGNS 60
QY 61 MVAIYAYKKQRTKTDVYIINLAVALDLLFTLPFMAVNAVHGVIGKIMCKITSALYT 120

Db 61 MVVAIYAYKKORTDVIYIIINLAVADLLFTLPFMAVNAVHGVIGKIMCKITSAIYT 120

QY 121 LNFVSGMOFLACISIDRYVAATKVPSSQGVGKPCMIICFCVMAAILISIPQLVFTVND 180

Db 121 LNFVSGMOFLACISIDRYVAATKVPSSQGVGKPCMIICFCVMAAILISIPQLVFTVND 180

QY 181 NARCIPFPFRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKKISRLK 240

Db 181 NARCIPFPFRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKKISRLK 240

QY 241 VLLTVVIVFIVTQLPYNTVKEFCRAIDIIYSLSITSCMSKMDIAIQTESIALFHSCLNP 300

Db 241 VLLTVVIVFIVTQLPYNTVKEFCRAIDIIYSLSITSCMSKMDIAIQTESIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVVKVAKKYGSRORQSVYEEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVVKVAKKYGSRORQSVYEEFPDSEGPTEPTSTFSI 350

RESULT 5

AAU08994

ID AAU08994 standard; protein; 350 AA.

AC AAU08994;

XX

DT 18-DEC-2001 (first entry)

DE Human G protein-coupled receptor, GPCR, 2398.

XX

KM Human; GPCR; G protein-coupled receptor; 2398; cardiac; antiatherosclerotic; analgesic; cytosolic; antiangiogenic; cardiovascular disorder; angiogenesis-related disorder; neural disorder; pain response disorder; inflammatory disorder; atherosclerosis; angina pectoris; myocardial infarction; ischaemic heart disease; sudden cardiac death; obesity; hypertensive heart disease; diabetes; prostate cancer-related pain.

KM

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT Region 125..141

FT /label=G_protein_receptor_signature

XX

XX WO200164882-A2.

XX

XX 07-SEP-2001.

XX

XX 28-FEB-2001; 2001MO-US006543.

XX

XX 29-FEB-2000; 2000US-0186059P.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Glucksmann MA, Galvin KM, Silos-Santiago I;

XX

XX WPI; 2001-589866/66.

XX

XX N-PSDB; AAS14572.

XX

XX Novel G protein coupled receptors and nucleic acids encoding them, for identifying agents for the treatment of cardiac disorders.

XX

PS Claim 9; Fig 9; 209pp; English.

XX

XX The invention relates to novel human G protein-coupled receptors (GPCR) named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and nucleic acids encoding them are useful for identifying agents for the treatment of cardiovascular disorders, angiogenesis-related disorders, neural disorders, pain response disorders and inflammatory disorders e.g. atherosclerosis, angina pectoris and myocardial infarction, ischaemic heart disease, sudden cardiac death, hypertensive heart disease, diabetes, prostate cancer-related pain, diabetes and obesity. The present sequence represents GPCR 2398

Seq Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;

Best Local Similarity 100.0%; Pred. No. 8.8e-195;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEONOSTDYENENNNQGYDYSQVELLIGIKEDVREFAVPLIPVELTIVFVGLAGNS 60

Db 1 MLEONOSTDYENENNNQGYDYSQVELLIGIKEDVREFAVPLIPVELTIVFVGLAGNS 60

QY 61 MVVAIYAYKKORTDVIYIIINLAVADLLFTLPFMAVNAVHGVIGKIMCKITSAIYT 120

Db 61 MVVAIYAYKKORTDVIYIIINLAVADLLFTLPFMAVNAVHGVIGKIMCKITSAIYT 120

QY 121 LNFVSGMOFLACISIDRYVAATKVPSSQGVGKPCMIICFCVMAAILISIPQLVFTVND 180

Db 121 LNFVSGMOFLACISIDRYVAATKVPSSQGVGKPCMIICFCVMAAILISIPQLVFTVND 180

QY 181 NARCIPFPFRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKKISRLK 240

Db 181 NARCIPFPFRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKKISRLK 240

QY 241 VLLTVVIVFIVTQLPYNTVKEFCRAIDIIYSLSITSCMSKMDIAIQTESIALFHSCLNP 300

Db 241 VLLTVVIVFIVTQLPYNTVKEFCRAIDIIYSLSITSCMSKMDIAIQTESIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVVKVAKKYGSRORQSVYEEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVVKVAKKYGSRORQSVYEEFPDSEGPTEPTSTFSI 350

RESULT 6

AAG80119

ID AAG80119 standard; protein; 350 AA.

AC AAG80119;

XX

DT 17-JAN-2002 (first entry)

DE Human CCR11 protein.

XX

KM Chemokine; tumor diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytotoxic; antiinflammatory; antiaesthetic; immunosuppressive; dermatological; antineumatic; antidiabetic.

KM

XX

XX Homo sapiens.

XX

XX WO200172830-A2.

XX

XX 04-OCT-2001.

XX

XX 02-APR-2001; 2001MO-EP003708.

XX

XX 31-MAR-2000; 2000DE-01016013.

XX

XX (TFP-) TFP PHARM GMBH.

XX

XX (FORS/) FORSMANN U.

XX

XX Forssmann W, Adernann K, Heitland A, Spodsberg N;

XX

XX WPI; 2001-626256/72.

XX

XX Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.

XX

XX Disclosure; Page 11; 26pp; German.

XX

XX This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal

CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (1) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiaesthetic,
 CC immunosuppressive, dermatological, antineumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80945-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;
 Best Local Similarity 100.0%; Pred. No. 8.8e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENKNGTDYSGYELICKEVDREFAKVLPEFLTVFVIGLAGNS 60
 DB 1 MALEQNSTDYEEENKNGTDYSGYELICKEVDREFAKVLPEFLTVFVIGLAGNS 60
 QY 61 MVAIAIYAYKKORTKDVYILNLAVADLLFLPFWANAVHGWLGKIMCKITSAIYT 120
 DB 61 MVAIAIYAYKKORTKDVYILNLAVADLLFLPFWANAVHGWLGKIMCKITSAIYT 120
 QY 121 LNFVSGMGFLACISIDRYAVATKVPSSQGVKPCWIIICFWMAAILLSIPOLVFYTVND 180
 DB 121 LNFVSGMGFLACISIDRYAVATKVPSSQGVKPCWIIICFWMAAILLSIPOLVFYTVND 180
 QY 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLMGVCYFTATLMKMPKISRPLK 240
 DB 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLMGVCYFTATLMKMPKISRPLK 240
 QY 241 VLTFTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDAIOVTESIALFHSCLNP 300
 DB 241 VLTFTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDAIOVTESIALFHSCLNP 300
 QY 301 ILVYFMGASFKNYVMKVAKKYGSRROROSVEEFPDSEGPTEPTSTFSI 350
 DB 301 ILVYFMGASFKNYVMKVAKKYGSRROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 7
 AAG67237

ID AAG67237 standard; protein; 350 AA.

AC AAG67237;

DT 13-NOV-2001 (first entry)

DE Amino acid sequence of human chemokine receptor CCR11.

KX Human; chemokine receptor; CCR11; G protein coupled receptor;
 KX inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
 KX asthma; angiogenesis; atherosclerosis vascular association disease;
 KX hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
 KX left ventricular diastolic dysfunction; migraine; preterm labour;
 KX oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
 KX myocardial infarction; congestive heart failure; endometriosis;
 KX vasospasm; retinopathy; nephropathy; pulmonary vascular disease.

OS Homo sapiens.

PN WO200166598-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US007073.

PR 03-MAR-2000; 2000US-0186928P.

PR 03-MAR-2000; 2000US-0187231P.

XX (ICOS-) ICOS CORP.

PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;

XX WPI; 2001-541918/60.

DR N-PSDS; AAH77711.

PT An isolated polynucleotide encoding the chemokine receptor CCR11, useful
 PT for treating rheumatoid arthritis, inflammatory bowel disease, asthma,
 PT angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's phenomenon
 PT and migraine.

XX Claim 13; Page 96-97; 110pp; English.

XX The present sequence represents the human chemokine receptor CCR11. CCR11
 CC is a member of the G protein coupled receptor family. A CCR11
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
 CC expression or biological activity, is useful for treating many
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
 CC bowel disease, and asthma. They are also useful for treating
 CC angiogenesis, atherosclerosis vascular association diseases which may
 CC include but are not limited to hypertension, angina pectoris, cardiac
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive heart
 CC failure, endometriosis, vasospasm, retinopathy, nephropathy, or pulmonary
 CC vascular disease

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;
 Best Local Similarity 100.0%; Pred. No. 8.8e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENKNGTDYSGYELICKEVDREFAKVLPEFLTVFVIGLAGNS 60
 DB 1 MALEQNSTDYEEENKNGTDYSGYELICKEVDREFAKVLPEFLTVFVIGLAGNS 60
 QY 61 MVAIAIYAYKKORTKDVYILNLAVADLLFLPFWANAVHGWLGKIMCKITSAIYT 120
 DB 61 MVAIAIYAYKKORTKDVYILNLAVADLLFLPFWANAVHGWLGKIMCKITSAIYT 120
 QY 121 LNFVSGMGFLACISIDRYAVATKVPSSQGVKPCWIIICFWMAAILLSIPOLVFYTVND 180
 DB 121 LNFVSGMGFLACISIDRYAVATKVPSSQGVKPCWIIICFWMAAILLSIPOLVFYTVND 180
 QY 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLMGVCYFTATLMKMPKISRPLK 240
 DB 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLMGVCYFTATLMKMPKISRPLK 240
 QY 241 VLTFTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDAIOVTESIALFHSCLNP 300
 DB 241 VLTFTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDAIOVTESIALFHSCLNP 300
 QY 301 ILVYFMGASFKNYVMKVAKKYGSRROROSVEEFPDSEGPTEPTSTFSI 350
 DB 301 ILVYFMGASFKNYVMKVAKKYGSRROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 8
 AAE37348

ID AAE37348 standard; protein; 350 AA.

AC AAE37348;

DT 27-AUG-2003 (first entry)

DE Human C-C chemokine receptor type 11 (CC CKR-11), 2398 protein.

XX Human; cardiovascular disorder; coronary artery disease; bradycardia;
 KW restenosis; cardiac hypertrophy; ischaemia reperfusion injury; angina;

arteriosclerosis; coronary artery ligation; rheumatic heart disease; heart failure; hypertension; cardiomyopathy; myocardial infarction; arterial inflammation; microembolism; atherosclerosis; endocarditis; vascular heart disease; valvular disease; arrhythmia; gene therapy; sinus node dysfunction; C-C chemokine receptor type 11; CC CKR-11; receptor.

XX Homo sapiens.

OS MO2003039341-A2.

XX PD 15-MAY-2003.

XX PF 05-NOV-2002; 2002MO-US035538.

XX PR 05-NOV-2001; 2001US-0339582P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Logan TJ, Chun M, Galvin KM;

XX DR WPI; 2003-441437/41.

XX DR N-PSDB; AAD56515.

XX PT Treating a subject having a cardiovascular disorder, e.g. angina, arrhythmia, or restenosis, comprises administering a 139, 258, 1261, 1486, 2398, 2414, 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or 93804 modulator.

XX PT 93804 modulator.

XX PS Disclosure; Page 105-106; 124pp; English.

XX CC The invention relates to methods and compositions for treating a subject having a cardiovascular disorder using 139, 258, 1261, 1486, 2398, 2414, 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or 93804 modulator. The invention is useful for treating a cardiovascular disorder, including arteriosclerosis, atherosclerosis, vascular wall remodeling, restenosis, cardiac hypertrophy, ischemia reperfusion injury, arterial inflammation, ventricular remodeling, rapid ventricular pacing, tachycardia, coronary microembolism, bradycardia, pressure overload, aortic bending, coronary artery ligation, vascular heart disease, valvular disease, including but not limited to, valvular degeneration caused by calcification, rheumatic heart disease, endocarditis, or complications of artificial valves; atrial fibrillation, long-QT syndrome, congestive heart failure, sinus node dysfunction, angina, heart failure, hypertension, atrial flutter, atrial fibrillation, pericardial disease, including but not limited to pericardial effusion and pericarditis, cardiomyopathies (e.g. dilated cardiomyopathy or idiopathic cardiomyopathy), myocardial infarction, coronary artery disease, coronary artery spasm, ischemic disease, arrhythmia, sudden cardiac death, and cardiovascular developmental disorders. The invention is also useful in gene therapy. The present sequence is human C-C chemokine receptor type 11 (CC CKR-11) protein. This sequence is used to illustrate the method of the invention

XX CC Sequence 350 AA;

XX SQ

Query Match 100.0%; Score 1819; DB 6; Length 350;

Best Local Similarity 100.0%; Pred. No. 8.8e-195;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSDYDYENENNGTGYDYOYLICKEDREFAKVPVPLTIVFVGLGNS 60

DB 1 MALEONOSDYDYENENNGTGYDYOYLICKEDREFAKVPVPLTIVFVGLGNS 60

QY 61 MVAIAVAYKKORTKTDVYIINLAVADLLFTLPFMAVNAVHGVIGIKICKITSALT 120

DB 61 MVAIAVAYKKORTKTDVYIINLAVADLLFTLPFMAVNAVHGVIGIKICKITSALT 120

QY 121 LNFVSGMOPLACISIDRYAVAVTKVPSOSGVKPCWIIICFCWMAAILISIQVLYTND 180

DB 121 LNFVSGMOPLACISIDRYAVAVTKVPSOSGVKPCWIIICFCWMAAILISIQVLYTND 180

QY 181 NARCIPIFRYVGTSMKALIQMLEICIGVFPILMGVCYFTARTLMKMNKISRLK 240

DB 181 NARCIPIFRYVGTSMKALIQMLEICIGVFPILMGVCYFTARTLMKMNKISRLK 240

DB 181 NARCIPIFRYVGTSMKALIQMLEICIGVFPILMGVCYFTARTLMKMNKISRLK 240

QY 241 VLLTVVIVFTVLTQLPYNIIVKFCRAIDIIYSILTSCKMKMDIAIQVTSIALFHSCLNP 300

DB 241 VLLTVVIVFTVLTQLPYNIIVKFCRAIDIIYSILTSCKMKMDIAIQVTSIALFHSCLNP 300

QY 301 ILVFMGASFKNYVVKAKKGSWROROSVEEPFDESGPEPTSTSI 350

DB 301 ILVFMGASFKNYVVKAKKGSWROROSVEEPFDESGPEPTSTSI 350

RESULT 9

ABP81716

ID ABP81716 standard; protein; 350 AA.

XX AC ABP81716;

XX DT 04-MAR-2003 (first entry)

XX DE Human C-C chemokine receptor 11 protein SEQ ID NO:607.

XX CC G protein-coupled receptor, GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; autoimmune disease; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer.

XX OS Homo sapiens.

XX SN WO200261087-A2.

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001MO-US050107.

XX PR 19-DEC-2000; 2000US-0257144P.

XX PI (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burner GC, Roush CL, Brown JP;

XX DR WPI; 2003-046718/04.

XX DR N-PSDB; ABZ42562.

XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

XX PT Disclosure; Fig 1; 523pp; English.

XX PS The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCR and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative disease, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242669 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 6; Length 350;

Best Local Similarity 100.0%; Pred. No. 8.8e-195; Indels 0; Gaps 0;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYVEENENMGTYDSQYELICTKEDVREFAKFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEQNSTDYVEENENMGTYDSQYELICTKEDVREFAKFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAATYAYKKQRTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITTSALYT 120
 DB 61 MVAATYAYKKQRTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITTSALYT 120
 QY 121 LNFVSGMQFLACISIDRYVAATKVPSSQGVGKPCWIIICFCVMAAILLSIPOLVPTVND 180
 DB 121 LNFVSGMQFLACISIDRYVAATKVPSSQGVGKPCWIIICFCVMAAILLSIPOLVPTVND 180
 QY 181 NARCIPIPRVYIGTSMKALIQMLEICIGFVVPFLMGVCYFITARLTMKMPNIXSRPLK 240
 DB 181 NARCIPIPRVYIGTSMKALIQMLEICIGFVVPFLMGVCYFITARLTMKMPNIXSRPLK 240
 QY 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 QY 301 ILVYMGASFKNYVMKAKKYGSMRQROSVBEPPDSGPTPEPTSTSI 350
 DB 301 ILVYMGASFKNYVMKAKKYGSMRQROSVBEPPDSGPTPEPTSTSI 350

RESULT 10

ID ADA10754 standard; protein; 350 AA.

AC ADA10754;

DT 06-NOV-2003 (first entry)

XX Human signal peptide, containing protein SP-16 Incyte 2547007.

XX human; signal peptide, containing protein; cell proliferation disorder;

KM cell signaling disorder; Huntington's disease; stomach cancer;

KM uterine cancer; mucinous cystadenoma; arthritis; testicular seminoma;

KM prostate cancer; bladder cancer; renal cell cancer; schizophrenia;

KM asthma; cancer.

XX Homo sapiens.

OS US2003073162-A1.

XX 17-APR-2003.

XX 01-OCT-2001; 2001US-00968433.

XX 07-NOV-1997; 97US-00966316.

XX 17-MAR-1999; 99US-00271110.

XX (LALP/) LAL P. G.

XX (AUTO/) AU-YOUNG J.

XX (REDD/) REDDY R.

XX (MURR/) MURRY L. E.

XX (MATH/) MATHUR P.

XX LAL P.G., Au-Young J., Reddy R., Murry LE, Mathur P;
 PI WPI; 2003-567307/53.
 XX N-PSDB; ADA10755.

PT New signal peptide-containing proteins and nucleic acids, useful in
 PT diagnosing, prognosing, treating or evaluating therapies for disorders
 PT associated with cell proliferation and cell signaling.

XX Claim 1; Fig 1; 59pp; English.

XX The invention relates to a new purified signal peptide-containing
 CC protein. The signal peptide-containing proteins and nucleic acids
 CC encoding them are useful in diagnosing, prognosing, treating or
 CC evaluating therapies for disorders associated with cell proliferation and
 CC cell signaling such as Huntington's disease, stomach cancer, uterine
 CC cancer, mucinous cystadenoma, arthritis, testicular seminoma, prostate
 CC cancer, bladder cancer, renal cell cancer, schizophrenia, asthma and
 CC cancer. The nucleic acids may be used in hybridisation, amplification and
 CC screening technologies to identify and distinguish among the identical
 CC and related molecules in a sample and to produce transgenic cell lines or
 CC organisms which are model systems for cancers and upon which the toxicity
 CC and efficacy of potential therapeutic treatments may be tested. The
 CC present sequence represents the amino acid sequence of a human signal
 CC peptide containing protein.

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 7; Length 350;

Best Local Similarity 100.0%; Pred. No. 8.8e-195; Indels 0; Gaps 0;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYVEENENMGTYDSQYELICTKEDVREFAKFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEQNSTDYVEENENMGTYDSQYELICTKEDVREFAKFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAATYAYKKQRTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITTSALYT 120
 DB 61 MVAATYAYKKQRTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITTSALYT 120
 QY 121 LNFVSGMQFLACISIDRYVAATKVPSSQGVGKPCWIIICFCVMAAILLSIPOLVPTVND 180
 DB 121 LNFVSGMQFLACISIDRYVAATKVPSSQGVGKPCWIIICFCVMAAILLSIPOLVPTVND 180
 QY 181 NARCIPIPRVYIGTSMKALIQMLEICIGFVVPFLMGVCYFITARLTMKMPNIXSRPLK 240
 DB 181 NARCIPIPRVYIGTSMKALIQMLEICIGFVVPFLMGVCYFITARLTMKMPNIXSRPLK 240
 QY 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 QY 301 ILVYMGASFKNYVMKAKKYGSMRQROSVBEPPDSGPTPEPTSTSI 350
 DB 301 ILVYMGASFKNYVMKAKKYGSMRQROSVBEPPDSGPTPEPTSTSI 350

RESULT 11

ID AAB62389 standard; protein; 382 AA.

XX AAB62389;

XX 29-JUN-2001 (first entry)

XX Human chemokine receptor CCX CKR polypeptide.

KM Chemokine receptor; CCX CKR; chemokine; ELC, SLG, TECK; modulator;

KM anti-inflammatory; immunosuppressive; cytostatic; antiallergic; human;

XX immunostimulant; gene therapy.

XX Homo sapiens.

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XX Key Location/Qualifiers
FH MISC-difference 351 /note= "encoded by TAA"
FT MISC-difference 353 /note= "encoded by TAA"
FT MISC-difference 365 /note= "encoded by TAA"
FT MISC-difference 371 /note= "encoded by TGA"
FT MISC-difference 371 /note= "encoded by TAA"
XX W0200127146-A2.
XX 19-APR-2001.
XX 10-OCT-2000; 2000MO-US028067.
XX 12-OCT-1999; 99US-0159015P.
XX 13-OCT-1999; 99US-0159210P.
XX 20-DEC-1999; 99US-0172979P.
XX 28-DEC-1999; 99US-0173388P.
XX 03-MAR-2000; 2000US-018662EP.
XX (CHEM-) CHEMOCENTRIX INC.
XX Goeligh J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
XX WPI; 2001-281975/29.
XX N-PSDB; AAF57685.
XX Isolated or recombinant chemokine receptor (designated CCX CR)
XX polypeptide (P1) or its fragment, useful for identifying CCX CR
XX modulators which can be used in the treatment of inflammation, allergy,
XX an autoimmune disease or cancer.
XX Claim 4; Fig 1; 72pp; English.
XX The invention relates to an isolated or recombinant chemokine receptor
XX designated CCX CR) polypeptide which binds to chemokines such as ELC,
XX SLK or TRBK. The CCX CR polypeptide is useful for identifying CCX CR
XX modulators. An agent that modulates the activity or expression of CCX CR
XX in a cell or tissue in the mammal is useful in the treatment of a CCX CR
XX mediated condition such as inflammation, allergy, an autoimmune disease,
XX graft rejection, cancer, an infectious disease or an immunosuppressive
XX disease. The present sequence represents the human CCX CR polypeptide
XX sequence 382 AA;
XX
XX Query Match 100.0%; Score 1819; DB 4; Length 382;
XX Best Local Similarity 100.0%; Pred. No. 9.8e-195;
XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MALEONOSTDYVYENENAGTYDYSOYELICIKEDVEPAKVPFLVPLTIVFVIGLAGNS 60
XX 1 MALEONOSTDYVYENENAGTYDYSOYELICIKEDVEPAKVPFLVPLTIVFVIGLAGNS 60
XX 1 MALEONOSTDYVYENENAGTYDYSOYELICIKEDVEPAKVPFLVPLTIVFVIGLAGNS 60
XX 61 MVAIAYAYKKQRTDYIINLAVALDILLFLPMAVNAHGVIGKIMCKITSLALT 120
XX 61 MVAIAYAYKKQRTDYIINLAVALDILLFLPMAVNAHGVIGKIMCKITSLALT 120
XX 61 MVAIAYAYKKQRTDYIINLAVALDILLFLPMAVNAHGVIGKIMCKITSLALT 120
XX 61 MVAIAYAYKKQRTDYIINLAVALDILLFLPMAVNAHGVIGKIMCKITSLALT 120
XX 121 LNFSWGMFLACISIDRYAVATKVPSSGVGKPCWICFCVMAAILLSIPOLVFTVND 180
XX 121 LNFSWGMFLACISIDRYAVATKVPSSGVGKPCWICFCVMAAILLSIPOLVFTVND 180
XX 121 LNFSWGMFLACISIDRYAVATKVPSSGVGKPCWICFCVMAAILLSIPOLVFTVND 180
XX 121 LNFSWGMFLACISIDRYAVATKVPSSGVGKPCWICFCVMAAILLSIPOLVFTVND 180
XX 181 NARCIPIPRYLGSMKALIMLEICIGFVVPFLIMGVCFITARTIMKMNINISPLK 240
XX 181 NARCIPIPRYLGSMKALIMLEICIGFVVPFLIMGVCFITARTIMKMNINISPLK 240
XX 181 NARCIPIPRYLGSMKALIMLEICIGFVVPFLIMGVCFITARTIMKMNINISPLK 240
XX 181 NARCIPIPRYLGSMKALIMLEICIGFVVPFLIMGVCFITARTIMKMNINISPLK 240
XX 241 VLTAVYIFITQUPYNIVKRCRAIDITYSITSONSKRMDIAQVTESTALFHSCLNP 300
XX 241 VLTAVYIFITQUPYNIVKRCRAIDITYSITSONSKRMDIAQVTESTALFHSCLNP 300
XX 241 VLTAVYIFITQUPYNIVKRCRAIDITYSITSONSKRMDIAQVTESTALFHSCLNP 300
XX 301 ILVFMGASPKNYVMKAKYGSWRKROSVSEFPSEGPTEPTSTFSI 350
XX 301 ILVFMGASPKNYVMKAKYGSWRKROSVSEFPSEGPTEPTSTFSI 350

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DB 301 ILVFMGASPKNYVMKAKYGSWRKROSVSEFPSEGPTEPTSTFSI 350
RESULT 12
AAW931170
ID AAW931170 standard; protein; 349 AA.
XX AAW931170;
XX 24-MAY-1999 (first entry)
XX Human HPIAO41 protein.
XX HPIAO41, G-coupled receptor; disease susceptibility; diagnosis; immunise;
XX treatment; HPIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
XX inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
XX diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
XX hypertension; hypertension; urinary retention; osteoporosis; allergy;
XX benign prostatic hyperplasia; myocardial infarction; ulcer; asthma; schizophrenia;
XX anxiety; manic depression; delirium; dementia; severe mental retardation;
XX dyslexia; Huntington's disease; Gilles de la Tourette's syndrome;
XX linkage analysis; gene mapping; human; ss.
XX Homo sapiens.
XX EP899332-A2.
XX 03-MAR-1999.
XX 17-FEB-1998; 98EP-00301170.
XX 15-AUG-1997; 97US-0055895P.
XX 27-OCT-1997; 97US-00962922.
XX (SMK) SMITHKLINE BEECHAM CORP.
XX Ellis CE;
XX WPI; 1999-144803/13.
XX N-PSDB; AAZ22558.
XX New G-coupled receptor (HPIAO41) polypeptide and polynucleotide - useful
XX as diagnostic reagents and for prevention and treatment of cancer, HIV
XX infections and Parkinson's disease.
XX Disclosure; Page 25-26; 27pp; English.
XX This sequence encodes a G-coupled receptor, HPIAO41 which is useful for
XX diagnosing susceptibility to diseases by detecting mutations in the
XX HPIAO41 gene, and can diagnose diseases associated with HPIAO41 protein
XX imbalance by determining HPIAO41 polypeptide expression levels. Agonists
XX and antagonists of the protein can be used in treatment to activate
XX (agonist) or inhibit (antagonist) HPIAO41 activity. In addition to direct
XX administration of antisense sequences to prevent expression, or HPIAO41
XX polynucleotides to treat conditions associated with a lack of HPIAO41
XX protein. Gene therapy may also be used to affect endogenous HPIAO41
XX polypeptide expression. HPIAO41 antibodies are useful for inducing an
XX immune response to immunise and prevent disease, and for isolating
XX HPIAO41 clones or purifying the polypeptides by affinity chromatography.
XX HPIAO41 clones or purifying the polypeptides by affinity chromatography.
XX inoculate against disease. Diseases diagnosed, prevented and treated
XX include bacterial, fungal, protozoan and viral infections, particularly
XX HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
XX disease; acute heart failure; hypertension; hypertension; urinary
XX retention; osteoporosis; benign prostatic hyperplasia; myocardial infarction;
XX asthma; allergies; benign prostatic hyperplasia; and psychotic and
XX neurological disorders, including anxiety, schizophrenia, manic
XX depression, delirium, dementia, severe mental retardation and dyslexias
XX such as Huntington's disease or Gilles de la Tourette's syndrome. The
XX HPIAO41 polypeptide is also useful for mapping the gene to a chromosome,
XX allowing gene inheritance to be studied through linkage analysis

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XX Sequence 349 AA;
 Query Match 99.7%; Score 1814; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3,2e-194;
 Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEONQSTDYEEENKGTVDYSGYELICKEVDREFAKFLPVFLTVFVIGLAGNSM 61
 DB 1 ALEONQSTDYEEENKGTVDYSGYELICKEVDREFAKFLPVFLTVFVIGLAGNSM 60
 QY 62 VVAIAIYKQKRTKDVIILMLAVADLLFLTFPMWANAAGWLGKIMKITSALYT 121
 DB 61 VVAIAIYKQKRTKDVIILMLAVADLLFLTFPMWANAAGWLGKIMKITSALYT 120
 QY 122 NFVSGMOFLACISIDRYAVATKVPQSGVGKPCWICFCVMAAILLSIPOLVFTYVND 181
 DB 121 NFVSGMOFLACISIDRYAVATKVPQSGVGKPCWICFCVMAAILLSIPOLVFTYVND 180
 QY 182 ARCTIPFRYLGTSKALIQMLEICIGFVFPFLMGVCYFTTARTLMKMPNIXSRPLK 241
 DB 181 ARCTIPFRYLGTSKALIQMLEICIGFVFPFLMGVCYFTTARTLMKMPNIXSRPLK 240
 QY 242 LITVIVIVITQLPYNIVKFCRAIDIIYSLTSCMSKRMIDIAIQVESIALFHSCLNPI 301
 DB 241 LITVIVIVITQLPYNIVKFCRAIDIIYSLTSCMSKRMIDIAIQVESIALFHSCLNPI 300
 QY 302 LYVFMGASFKNYVMKVAKKYGSWRQROSVVEFPDSEGPTEPTSTFSI 350
 DB 301 LYVFMGASFKNYVMKVAKKYGSWRQROSVVEFPDSEGPTEPTSTFSI 349

RESULT 13
 ID AAY30125 standard; protein; 350 AA.
 AC AAY30125;
 XX
 DT 14-OCT-1999 (first entry)
 XX
 DE A human seven-pass transmembrane receptor protein.
 XX
 KW Seven-pass transmembrane receptor; autoimmune disease;
 KM white blood cell dysfunction.
 XX
 OS Homo sapiens.
 OS
 PN WO933876-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 24-DEC-1998; 98MO-JP005886.
 XX
 PR 24-DEC-1997; 97JP-00354537.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Ohno T, Koshio T, Ishimaru H;
 XX
 DR WPI: 1999-493806/41.
 DR N-PSDB; AA86674.
 XX
 PT New seven-pass transmembrane receptor protein useful for treating,
 XX preventing or diagnosing autoimmune diseases.
 XX
 PS Claim 1, Page 101-103; 118pp; Japanese.
 XX
 CC The present sequence represents a seven-pass transmembrane receptor
 CC protein. The protein and its DNA can be used to screen substances for the
 CC diagnosis, prevention and treatment of autoimmune diseases, particularly
 CC those due to white blood cell dysfunction
 XX
 SQ Sequence 350 AA;

QY 1 MALEONQSTDYEEENKGTVDYSGYELICKEVDREFAKFLPVFLTVFVIGLAGNS 60
 DB 1 MALEONQSTDYEEENKGTVDYSGYELICKEVDREFAKFLPVFLTVFVIGLAGNS 60
 QY 61 MVAIAIYKQKRTKDVIILMLAVADLLFLTFPMWANAAGWLGKIMKITSALYT 120
 DB 61 MVAIAIYKQKRTKDVIILMLAVADLLFLTFPMWANAAGWLGKIMKITSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPQSGVGKPCWICFCVMAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPQSGVGKPCWICFCVMAAILLSIPOLVFTYVND 180
 QY 181 NARCTIPFRYLGTSKALIQMLEICIGFVFPFLMGVCYFTTARTLMKMPNIXSRPLK 240
 DB 181 NARCTIPFRYLGTSKALIQMLEICIGFVFPFLMGVCYFTTARTLMKMPNIXSRPLK 240
 QY 241 VITVIVIVITQLPYNIVKFCRAIDIIYSLTSCMSKRMIDIAIQVESIALFHSCLNPI 300
 DB 241 VITVIVIVITQLPYNIVKFCRAIDIIYSLTSCMSKRMIDIAIQVESIALFHSCLNPI 300
 QY 301 LYVFMGASFKNYVMKVAKKYGSWRQROSVVEFPDSEGPTEPTSTFSI 350
 DB 301 LYVFMGASFKNYVMKVAKKYGSWRQROSVVEFPDSEGPTEPTSTFSI 350

RESULT 14
 ID AAB02835 standard; protein; 350 AA.
 AC AAB02835;
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Human G protein coupled receptor hPRL1 protein SEQ ID NO:24.
 XX
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 KM identification; agonist; screening; therapeutic; pharmaceutical; mutant.
 XX
 OS Homo sapiens.
 OS
 PN WC00022131-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99MO-US024065.
 XX
 PR 13-OCT-1998; 98US-01170496.
 XX
 PR 12-NOV-1998; 98US-0108029P.
 XX
 PR 27-NOV-1998; 98US-0109213P.
 XX
 PR 16-FEB-1999; 98US-0110060P.
 XX
 PR 26-FEB-1999; 99US-0120416P.
 XX
 PR 12-MAR-1999; 99US-0123944P.
 XX
 PR 12-MAR-1999; 99US-0123945P.
 XX
 PR 12-MAR-1999; 99US-0123946P.
 XX
 PR 12-MAR-1999; 99US-0123948P.
 XX
 PR 12-MAR-1999; 99US-0123949P.
 XX
 PR 12-MAR-1999; 99US-0123951P.
 XX
 PR 28-MAY-1999; 99US-0136436P.
 XX
 PR 28-MAY-1999; 99US-0136437P.
 XX
 PR 28-MAY-1999; 99US-0136439P.
 XX
 PR 28-MAY-1999; 99US-0137127P.
 XX
 PR 28-MAY-1999; 99US-0137131P.
 XX
 PR 28-MAY-1999; 99US-0137567P.
 XX
 PR 29-JUN-1999; 99US-0141448P.
 XX
 PR 27-AUG-1999; 99US-0151114P.
 XX
 PR 03-SEP-1999; 99US-0152524P.
 XX
 PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 29-SEP-1999; 99US-0156635P.
 PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157283P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.

XX (AREN-) ARENA PHARM INC.

PI Behan DP, Lehmann-Brunsmma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

XX WPI; 2000-317986/27.
 DR N-PSDB; AAA46029.

XX Non-endogenous, human G protein-coupled receptors for screening receptor,
 PT inverse or partial agonists useful as therapeutic agents.

XX Example 1; Page 99-100; 187pp; English.

XX The present invention describes transmembrane receptors, preferably human
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is
 CC unknown (orphan GPCR receptors). More specifically the present invention
 CC relates to non-endogenous, constitutively activated versions of a human
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct
 CC identification of candidate compounds as receptor agonists, inverse
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
 CC exemplification of the present invention

XX Sequence 350 AA;

XX Query Match 99.5%; Score 1810; DB 3; Length 350;
 XX Best Local Similarity 99.4%; Pred. No. 8.9e-194;

XX Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 M A L E N O S T D Y Y E N E N N G T Y D Y S Q Y E L I C K E D V R E F A K V L P V L T I V F I G L A G N S 60
 DB 1 M A L E N O S T D Y Y E N E N N G T Y D Y S Q Y E L I C K E D V R E F A K V L P V L T I V F I G L A G N S 60
 QY 61 M V A I Y A Y K K O R T D V Y I I N L A V A D L L F T L P F M A V N A H G M V L G K I M C K I T S A L Y T 120
 DB 61 M V A I Y A Y K K O R T D V Y I I N L A V A D L L F T L P F M A V N A H G M V L G K I M C K I T S A L Y T 120
 QY 121 L N F V S G M O F L A C I S I D R Y V A V T K V P S G S G V K P C W I I C F C W M A A I L I S I P O L V F Y T V N D 180
 DB 121 L N F V S G M O F L A C I S I D R Y V A V T K V P S G S G V K P C W I I C F C W M A A I L I S I P O L V F Y T V N D 180
 QY 181 N A R C P I P R Y L G T S M K A L I O M L E I C I G F V V P F I M G V C Y T I T A T K M N I K S R P L K 240
 DB 181 N A R C P I P R Y L G T S M K A L I O M L E I C I G F V V P F I M G V C Y T I T A T K M N I K S R P L K 240
 QY 241 V L L T V I V I F I T O L P Y N I V K F C R A I D I I Y S I T S C N S K R M D I A I Q V T E S I A L F H S C I N P 300
 DB 241 V L L T V I V I F I T O L P Y N I V K F C R A I D I I Y S I T S C N S K R M D I A I Q V T E S I A L F H S C I N P 300
 QY 301 I L Y V M G S F K N Y V M K V A K K Y G S W R O R O S V E E P F D S E G T E P T S T S I 350
 DB 301 I L Y V M G S F K N Y V M K V A K K Y G S W R O R O S V E E P F D S E G T E P T S T S I 350

XX RESULT 15

XX AA771301 standard; protein; 350 AA.

XX AA771301;

XX 02-NOV-2000 (first entry)

XX DT

XX XX

DE Human orphan G protein-coupled receptor hppr1.
 XX Human; orphan G protein-coupled receptor; GPCR; hppr1; drug screening;
 KM transmembrane receptor; expressed sequence tag; EST; signal cascade.

XX Homo sapiens.

XX MO200031258-A2.

XX 02-JUN-2000.

XX 13-OCT-1999; 99WO-US023687.

XX 20-NOV-1998; 98US-0109213P.

XX 16-FEB-1999; 99US-0120416P.

XX 26-FEB-1999; 99US-0121852P.

XX 12-MAR-1999; 99US-0123946P.

XX 12-MAR-1999; 99US-0123949P.

XX 28-MAY-1999; 99US-0136436P.

XX 28-MAY-1999; 99US-0136437P.

XX 28-MAY-1999; 99US-0136439P.

XX 28-MAY-1999; 99US-0136567P.

XX 28-MAY-1999; 99US-0137127P.

XX 29-JUN-1999; 99US-0141448P.

XX 29-SEP-1999; 99US-0156555P.

XX 29-SEP-1999; 99US-0156633P.

XX 29-SEP-1999; 99US-0156634P.

XX 29-SEP-1999; 99US-0156635P.

XX 01-OCT-1999; 99US-0157280P.

XX 01-OCT-1999; 99US-0157281P.

XX 01-OCT-1999; 99US-0157282P.

XX 01-OCT-1999; 99US-0157293P.

XX 01-OCT-1999; 99US-0157294P.

XX 12-OCT-1999; 99US-00416760.

XX 12-OCT-1999; 99US-00417044.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Liaw CW, Lin I;

XX WPI; 2000-400068/34.

XX N-PSDB; AAD01128.

XX Novel human orphan G protein-coupled receptors and the encoding cDNAs for
 PT use in the identification of G protein-coupled receptor agonists.

XX Claim 42; Page 69-70; 102pp; English.

XX The present amino acid sequence is the hppr1, an endogenous human orphan
 CC G protein-coupled receptor (GPCR), expressed in the pituitary gland,
 CC heart, salivary gland, small intestine and testis. The hppr1 cDNA was
 CC identified using EST (expressed sequence tag) AA359504 and 218667 as a
 CC probe. The orphan GPCR of the invention, like all GPCRs has seven
 CC transmembrane alpha helices with an extracellular N-terminus and an
 CC intracellular C-terminus. However, no endogenous ligands has yet been
 CC identified for the proteins of the invention. The orphan GPCRs may be
 CC used in the identification of their endogenous ligands, and to screen
 CC potential GPCR agonists and antagonists for use as pharmaceutical agents.
 CC The proteins may also be used in the study of GPCR-mediated signalling
 CC cascades, and to elucidate their precise role in normal and diseased
 CC human conditions. Nucleic acid encoding human orphan GPCRs may be used
 CC for tissue localisation expression analysis to provide information about
 CC their function in healthy and pathological states

XX Sequence 350 AA;

XX Query Match 99.5%; Score 1810; DB 3; Length 350;
 XX Best Local Similarity 99.4%; Pred. No. 8.9e-194;

XX Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 M A L E N O S T D Y Y E N E N N G T Y D Y S Q Y E L I C K E D V R E F A K V L P V L T I V F I G L A G N S 60
 DB 1 M A L E N O S T D Y Y E N E N N G T Y D Y S Q Y E L I C K E D V R E F A K V L P V L T I V F I G L A G N S 60

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QY	61	MVAIYAAYKKORTKDVIYILNLAVADLLFLPLPFMAVAVHGWVLGKIMCKITSALYT	120
Db	61	MVAIYAAYKKORTKDVIYILNLAVADLLFLPLPFMAVAVHGWVLGKIMCKITSALYT	120
QY	121	LNFSGMQPLACTSIDRYAVTVKVPQSQGVKPCWIIICCVMAAILLSIPOLVFTVND	180
Db	121	LNFSGMQPLACTSIDRYAVTVKVPQSQGVKPCWIIICCVMAAILLSIPOLVFTVND	180
QY	181	NARCIPIFPRIYLGTSKMLIOMLEICIGFVVPFLIMGVCYFTARTIMQPNIKISRPLX	240
Db	181	NARCIPIFPRIYLGTSKMLIOMLEICIGFVVPFLIMGVCYFTARTIMQPNIKISRPLX	240
QY	241	VLLTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP	300
Db	241	VLLTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP	300
QY	301	ILYVFMGASFKNYVMKVAKKYGSMSROROSVEEFPDSEGPTEPTSTPSI	350
Db	301	ILYVFMGASFKNYVMKVAKKYGSMSROROSVEEFPDSEGPTEPTSTPSI	350

Search completed: April 13, 2004, 13:17:34
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:20 ; Search time 23 Seconds

(without alignments)
785.613 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819
Sequence: 1 MALEONOSTDYEEENENG.....VEEPFSEGTPTSTPSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	US-08-966-316-16
2	1808	99.4	350	4	US-09-556-002-2
3	1620	89.1	350	2	US-08-966-316-18
4	659	36.2	358	1	US-08-153-848-19
5	659	36.2	358	3	US-09-299-843A-19
6	659	36.2	358	4	US-09-088-337B-19
7	659	36.2	358	5	PCT-US93-11153-19
8	659	36.2	378	1	US-08-153-848-15
9	659	36.2	378	3	US-09-299-843A-15
10	659	36.2	378	3	US-09-251-545-1
11	659	36.2	378	4	US-09-088-337B-15
12	659	36.2	378	4	US-09-170-496D-74
13	659	36.2	410	5	PCT-US93-11153-15
14	659	36.2	410	1	US-08-153-848-7
15	659	36.2	410	3	US-09-299-843A-7
16	659	36.2	410	5	US-09-088-337B-7
17	659	36.2	410	5	PCT-US93-11153-7
18	655	36.0	378	4	US-09-170-496D-204
19	650	35.7	378	3	US-09-299-843A-66
20	650	35.7	378	4	US-09-088-337B-66
21	643	35.3	378	1	US-08-383-750-2
22	643	35.3	378	1	US-08-383-751A-2
23	643	35.3	378	3	US-08-352-678-2
24	643	35.3	378	3	US-09-045-583-45
25	643	35.3	378	4	US-09-534-185-49
26	643	35.3	378	4	US-09-536-954-2
27	643	35.3	378	5	PCT-US93-09636-2

28	637	35.0	357	4	US-09-266-464-2	Sequence 2, Appl1
29	637	35.0	357	4	US-09-170-496D-24	Sequence 24, Appl1
30	635.5	34.9	359	1	US-08-153-848-24	Sequence 24, Appl1
31	635.5	34.9	359	3	US-09-299-843A-24	Sequence 24, Appl1
32	635.5	34.9	359	4	US-09-088-337B-24	Sequence 24, Appl1
33	635.5	34.9	359	5	PCT-US93-11153-24	Sequence 24, Appl1
34	631	34.7	357	4	US-09-170-496D-176	Sequence 176, App
35	606.5	33.3	361	2	US-08-902-294-2	Sequence 2, Appl1
36	606.5	33.3	361	3	US-09-178-637-2	Sequence 2, Appl1
37	583	32.1	374	3	US-09-045-583-48	Sequence 48, Appl1
38	583	32.1	374	4	US-09-534-185-48	Sequence 48, Appl1
39	581	31.9	342	3	US-09-116-498-4	Sequence 4, Appl1
40	569	31.3	342	2	US-09-116-498-6	Sequence 6, Appl1
41	560	30.8	342	2	US-08-742-011-2	Sequence 2, Appl1
42	560	30.8	342	3	US-09-275-384B-5	Sequence 5, Appl1
43	560	30.8	342	3	US-09-116-498-2	Sequence 2, Appl1
44	560	30.8	342	4	US-09-449-437A-2	Sequence 2, Appl1
45	560	30.8	342	4	US-09-517-605-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-08-966-316-16
Sequence 16, Application US/08966316
Patent No. 5932445
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murthy, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTMSNOT11
CLONE: 2547002
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.2e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENGTYSQYELICKEDEVEPAKFLPVLITIVIGLAGNS 60
DB 1 MALEONOSTDYEEENENGTYSQYELICKEDEVEPAKFLPVLITIVIGLAGNS 60
QY 61 MVAIAAYAYKKORTKTDVYIINLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALT 120
DB 61 MVAIAAYAYKKORTKTDVYIINLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALT 120
QY 121 INFVSGMOFLACISIDRYAVATKVPQSOGVGPCKWIIICFWMAAILISIPQLVFTYND 180
DB 121 INFVSGMOFLACISIDRYAVATKVPQSOGVGPCKWIIICFWMAAILISIPQLVFTYND 180
QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMNKISRPLX 240
DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMNKISRPLX 240
QY 241 VLLTVIVIFVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIALQVTSIALFHSCLNP 300
DB 241 VLLTVIVIFVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIALQVTSIALFHSCLNP 300
QY 301 ILVFMGASFKYVWVKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350
DB 301 ILVFMGASFKYVWVKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350

RESULT 2
US-09-556-002-2
; Sequence 2, Application us/09556002
; Patent No. 6620615
; GENERAL INFORMATION:
; APPLICANT: Gould-Rochberg, Bonnie
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR AND METHOD OF USING SAME
; FILE REFERENCE: 15966-550
; CURRENT APPLICATION NUMBER: US/09/556,002
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: USSN 60/130,817
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-556-002-2

Query Match 99.4%; Score 1808; DB 4; Length 350;
Best Local Similarity 99.4%; Pred. No. 1.1e-147;
Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 61 MVAIAAYAYKKORTKTDVYIINLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALT 120
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DB 121 INFVSGMOFLACISIDRYAVATKVPQSOGVGPCKWIIICFWMAAILISIPQLVFTYND 180
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QY 241 VLLTVIVIFVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIALQVTSIALFHSCLNP 300
DB 241 VLLTVIVIFVITQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIALQVTSIALFHSCLNP 300

QY 301 ILVFMGASFKYVWVKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350
DB 301 ILVFMGASFKYVWVKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350

RESULT 3
US-08-966-316-18
; Sequence 18, Application us/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: P2-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 399711
US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.5e-131;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENGTYSQYELICKEDEVEPAKFLPVLITIVIGLAGNS 60
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DB 61 MVAIAAYAYKKORTKTDVYIINLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALT 120
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DB 121 INFVSGMOFLACISIDRYAVATKVPQSOGVGPCKWIIICFWMAAILISIPQLVFTYND 180
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DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMNKISRPLX 240

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DB 181 KACACVIFPHYHGTSGKASIQLEICIGPIIPFLMAVCYFTTAKTLIMPNIKKSOPK 240
QY 241 VLTIVIVIVITVQLPKNIVKFCRAIDIIYSILITSCNMSKRDIAIQVTEISILFSCNLP 300
DB 241 VLTIVIVIVITVQLPKNIVKFCRAIDIIYSILITSCNMSKRDIAIQVTEISILFSCNLP 300
QY 301 ILVFMGASFKNVKVMKAKKYGSMRQROSVDEFPDSEGPTEPTSTFSI 350
DB 301 VLVFMGTSFKNYIMKVKAKKYGSMRQROSVDEFPDSEGPTEPTSTFSI 350

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RESULT 4
US-08-153-848-19

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/ Sequence 19, Application US/08153848
/ Patent No. 5759804
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schweikart, Vicki L.
/ TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 64
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ STEEN: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/153,848
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5759804and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 31794
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 358 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-153-848-19

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Query Match 36.2%; Score 659; DB 1; Length 358;
Best Local Similarity 38.7%; Pred. No. 5.1e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY 1 MALEQNSQSDIYYEENMGTYISQYELICIKEDYREZAKFLPVFLTIIVIGLAQNS 60
DB 1 VCLCQDEVDYDYGNT--TVDYTLFESLCSKRDYRANKAMFLPMYSIIFVGLNG 57
QY 61 MVVAIAYYKQRTKTDVYILNLAIVADLLFLTPFWAVNAVAGWLGKIMCKITSALYT 120
DB 58 LVVLTIVIVITVQLPKNIVKFCRAIDIIYSILITSCNMSKRDIAIQVTEISILFSCNLP 117
QY 121 LNFVSGNOLACTISIRRYAVTKVPS---QSGVKGPCWIIICPCVMAAILISIQLYY 176
DB 118 MSFSGMLLLLCISIDRYVAIVAVASAHRRFARVLLISXLSGVGIWIIATVLSIPELLYS 177

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QY 177 TVNDNA-----RCIPRPVYLGSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKP 231
DB 178 DLQSSSEQAMRGLINEH---VEAFITQVAGVIGFVPLLAMSFCYLVIRITLLQAR 234
QY 232 NIKSRPLKLLLVIVITVQLPKNIVKFCRAIDIIYSILITSCNMSKRDIAIQVTEIS 291
DB 235 NFEENKAIKVIIAVVVFVIFQLPYNGVLAQTVANFNITSTCELSKQNLIAVDVYSL 294
QY 292 ALFHSCLNPLIYVFMGASFKNVKVMKAKKYG-----SW-----RROQSVDEFPD 337
DB 295 ACVACCVNPFYARIGVYFNDLFKFLKDGCLSGQLRQMSGRHRRASMSVE----- 349
QY 338 SEGPTEPTSTFS 349
DB 350 ---AETTTFS 357

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RESULT 5

US-09-299-843A-19

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/ Sequence 19, Application US/09299843A
/ Patent No. 6107475
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schweikart, Vicki L.
/ TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/299,843A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 09/086,337
/ FILING DATE: 01-JUN-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/153,848
/ FILING DATE: 17-NOV-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: J11 E. Uhl
/ REGISTRATION NUMBER: 43,213
/ REFERENCE/DOCKET NUMBER: 27866/32059B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 358 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-299-843A-19

```

Query Match 36.2%; Score 659; DB 3; Length 358;
Best Local Similarity 38.7%; Pred. No. 5.1e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY      1  M A L E O N S T D Y Y E N E M N G T Y D S O Y E L I C I K E D V R E P A K F L P V F L T I V F I G L A G N S 60
Db      1  V C L C O D E V T D D Y I G D N T - - - T V D Y T L F E S I C S K D V A N F K A M F L P I M Y S I I C F V G L I G N G 57
QY      61  M V A I A Y A Y K K O R K T D V Y I L N L A V A D L L L F T L P F A V A N A V H G W I G K I M C K I T S A L Y T 120
Db      58  L V L T Y I F K R K T M D T Y L N L A V A D I L F L T L P F A V S A A S W V G V H F C K L I F A I Y K 117
QY      121  L N F V S G M O F L A C I S I D R Y V A V T K V P S - - - Q S G V K P C W I C F C W M A A L I L S I P O L V F Y 176
Db      118  M S F S G M L L I C I S I D R Y V A I V Q A V S A H R R A V L I S K L S C V G I W I L A T V L S I P E L L Y S 177
QY      177  T V N D N A - - - R C I P I F P R Y I G T S M K A L I O M L E I C I G F V V P F L I M S G Y T I T A T I M K M P 231
Db      178  D L O R S S E Q A M R C S L I T E H - - - V E A F I T T I O V A Q W I G F L V P L A M S F C Y L V I T R T L L Q A R 234
QY      232  N I K I S R P L K V L T V V I V I T O L P N I V K F C R A I D I Y S L I T S C M S K R M D I A I Q V T E S I 291
Db      235  N F E R N K A I K V I A V V V F I V F O L P Y N G V L A Q T A N F N I T S T C E L S K O L N I A V D V Y S L 294
QY      292  A L F H S C L N P I L Y V M G A S F K N Y V M K V A K K Y G - - - S W - - - - - R R O R S V E E P F D 337
Db      295  A C V R C C N P F L Y A F I G V K F R N D L F K L F K D G C L S O E Q L R O M S G C R H I R S M S V E - - - - - 349
QY      338  S E G P T E P T S T F S 349
Db      350  - - - - - A E T T T T F S 357

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RESULT 6

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US-09-088-337B-19
Sequence 19, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids

```

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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-088-337B-19
Query Match 36.2%; Score 659; DB 4; Length 358;
Best Local Similarity 38.7%; Pred. No. 5,1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY      1  M A L E O N S T D Y Y E N E M N G T Y D S O Y E L I C I K E D V R E P A K F L P V F L T I V F I G L A G N S 60
Db      1  V C L C O D E V T D D Y I G D N T - - - T V D Y T L F E S I C S K D V A N F K A M F L P I M Y S I I C F V G L I G N G 57
QY      61  M V A I A Y A Y K K O R K T D V Y I L N L A V A D L L L F T L P F A V A N A V H G W I G K I M C K I T S A L Y T 120
Db      58  L V L T Y I F K R K T M D T Y L N L A V A D I L F L T L P F A V S A A S W V G V H F C K L I F A I Y K 117
QY      121  L N F V S G M O F L A C I S I D R Y V A V T K V P S - - - Q S G V K P C W I C F C W M A A L I L S I P O L V F Y 176
Db      118  M S F S G M L L I C I S I D R Y V A I V Q A V S A H R R A V L I S K L S C V G I W I L A T V L S I P E L L Y S 177
QY      177  T V N D N A - - - R C I P I F P R Y I G T S M K A L I O M L E I C I G F V V P F L I M S G Y T I T A T I M K M P 231
Db      178  D L O R S S E Q A M R C S L I T E H - - - V E A F I T T I O V A Q W I G F L V P L A M S F C Y L V I T R T L L Q A R 234
QY      232  N I K I S R P L K V L T V V I V I T O L P N I V K F C R A I D I Y S L I T S C M S K R M D I A I Q V T E S I 291
Db      235  N F E R N K A I K V I A V V V F I V F O L P Y N G V L A Q T A N F N I T S T C E L S K O L N I A V D V Y S L 294
QY      292  A L F H S C L N P I L Y V M G A S F K N Y V M K V A K K Y G - - - S W - - - - - R R O R S V E E P F D 337
Db      295  A C V R C C N P F L Y A F I G V K F R N D L F K L F K D G C L S O E Q L R O M S G C R H I R S M S V E - - - - - 349
QY      338  S E G P T E P T S T F S 349
Db      350  - - - - - A E T T T T F S 357

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RESULT 7

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PCT-US93-11153-19
Sequence 19, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-19

Query Match 36.2%; Score 659; DB 5; Length 358;
Best Local Similarity 38.7%; Pred. No. 5,4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSTDYEEENENNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
DB 1 VCLQDEVTDDYIDGNT---TVDYTLFESLCSKXDVNFKAMFLPIWYSIICFVGLGNG 57
QY 61 MVVAIAYKKQKRTKTDVYILNLAVALDLLFTLPFMAVNAHGWVLGKIMCKITSALYT 120
DB 58 LVVLTITFRKLTMTDYILNLAVALDLLFTLPFMAVSAKSWVGVHFKLIFAIYK 117
QY 121 LNFVSGNQFLACISIDRYAVATKVP---QSGVGKPCWICFCVMAAILISIPQLVY 176
DB 118 MSFSGMLLLCISIDRYAVATKVP---QSGVGKPCWICFCVMAAILISIPQLVY 176
QY 177 TVNDNA-----RCIPFPRYLGTSKALLQMLEICIGFVVPFLMGVCYITARTLMMP 231
DB 178 DLORSSSEQAMRCSLTER---VEAFITIQVQVIGFVPLPMAISFCVLIIRTLQAR 234
QY 232 NIKSRPLKYLTVIVITVITQLPYINIVKFCRAIDIIYSITSCMSKMDIAIQVTESI 291
DB 235 NFERNKAIKIIIAVAVVFIYFQLPYNGVLAQVANNITSTSCISKQNTAIADVTYSL 294
QY 292 ALFHSCLNPLIYVFGASFRNYVMKAKYK-----SW-----RRQGVSEEPFD 337
DB 295 ACVRCVNPFLYAFIVGKFRNDLFKFLKDLGCLSQEQLRQMSSCRHRRSSMSVE----- 349
QY 338 SEGTEPTSTPS 349
DB 350 ----AETTTTFS 357

RESULT 8
US-08-153-848-15
Sequence 15, Application US/08153848
Patent No. 5759804

GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-15

Query Match 36.2%; Score 659; DB 1; Length 378;
Best Local Similarity 38.7%; Pred. No. 5,4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSTDYEEENENNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
DB 21 VCLQDEVTDDYIDGNT---TVDYTLFESLCSKXDVNFKAMFLPIWYSIICFVGLGNG 77
QY 61 MVVAIAYKKQKRTKTDVYILNLAVALDLLFTLPFMAVNAHGWVLGKIMCKITSALYT 120
DB 78 LVVLTITFRKLTMTDYILNLAVALDLLFTLPFMAVSAKSWVGVHFKLIFAIYK 137
QY 121 LNFVSGNQFLACISIDRYAVATKVP---QSGVGKPCWICFCVMAAILISIPQLVY 176
DB 138 MSFSGMLLLCISIDRYAVATKVP---QSGVGKPCWICFCVMAAILISIPQLVY 176
QY 177 TVNDNA-----RCIPFPRYLGTSKALLQMLEICIGFVVPFLMGVCYITARTLMMP 231
DB 198 DLORSSSEQAMRCSLTER---VEAFITIQVQVIGFVPLPMAISFCVLIIRTLQAR 254
QY 232 NIKSRPLKYLTVIVITVITQLPYINIVKFCRAIDIIYSITSCMSKMDIAIQVTESI 291
DB 235 NFERNKAIKIIIAVAVVFIYFQLPYNGVLAQVANNITSTSCISKQNTAIADVTYSL 314
QY 292 ALFHSCLNPLIYVFGASFRNYVMKAKYK-----SW-----RRQGVSEEPFD 337
DB 315 ACVRCVNPFLYAFIVGKFRNDLFKFLKDLGCLSQEQLRQMSSCRHRRSSMSVE----- 369
QY 338 SEGTEPTSTPS 349
DB 370 ----AETTTTFS 377

RESULT 9
US-09-299-843A-15
Sequence 15, Application US/09299843A
Patent No. 6107475

GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25


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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-15

Query Match      36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 5,4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 M A L E Q N S T D Y Y E E N M N G T Y D S Q Y E L I C K E D Y R E F A K V L P V F L T I V F V I G L A G N S 60
DB 21 V C L C D E V T D D Y I G D N T --- T V D Y T L F E S L C S K D Y R N F K A M F L P I M S I I C F V G L L G N G 77

QY 61 M V T A I Y A Y K K O R T K T D V Y I I N L A V A D L L L F T L P F M A V N A V H G W L G K I M C K I T S A L Y T 120
DB 78 L V A L T Y I F E R K L T M D T Y L N L A V A D I L F L T L P F M A Y S A K S W F G V H F C K L I F A I Y K 137

QY 121 I N F V S G M Q F L A C I S I D R Y A V A V T K V P S --- Q S G V K P C W I I C F C V M A A I L I S P O L V E Y 176
DB 138 M S F F S G M L L I C I S I D R Y A I V A Q A V S A H R H R A R V L I S K S C V G I W I A T V L S I P E L L Y S 197

QY 177 T V N D N A --- R C I P F P R Y L G T S M K A L I O M L E I C I G F V P F L I N G V C Y F T A R T L M K P 231
DB 198 D L O R S S E Q A M R C S L I T E H --- V E A F I T I V A Q W I G F L V P L A M S F C Y L V I I R T L L Q A R 254

QY 232 N I K I S R P L K L T V V I V F I V T O L P Y N I V K F C R A I D I I Y S L I T S C M S K M D I A I Q Y T E S I 291
DB 255 N F E R N K A I K I I A V V V I F V F O L P Y N G V L A Q V A N F N I T S T C E L S K O L N I A D V T Y S L 314

QY 292 A L F H S C L N P L Y F E M G A S F K N Y M K V A K K Y G --- S W --- R R O S V E E P F P D 337
DB 315 A C V R C C V N P E L V A F I G V K F R N D L F K L F K D L G C L S Q E Q L R O W S C R H I R S S M S V E --- 369

QY 338 S E G P T E P T S F S 349
DB 370 --- A E T T T F S 377

RESULT 10
US-09-251-545-1
Sequence 1, Application US/09251545
Patent No. 6153441
GENERAL INFORMATION:
APPLICANT: Edward R. Appelbaum
APPLICANT: Henry M. Sarau
APPLICANT: John R. White
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
TITLE OF INVENTION: AND CCR7-9 LIGAND AND INTERACTION THEREOF

```

```

FILE REFERENCE: P50753
CURRENT APPLICATION NUMBER: US/09/251,545
CURRENT FILING DATE: 1999-02-17
EARLIER APPLICATION NUMBER: 60/074,883
EARLIER FILING DATE: 1998-02-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Human
US-09-251-545-1

Query Match      36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 5,4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 M A L E Q N S T D Y Y E E N M N G T Y D S Q Y E L I C K E D Y R E F A K V L P V F L T I V F V I G L A G N S 60
DB 21 V C L C D E V T D D Y I G D N T --- T V D Y T L F E S L C S K D Y R N F K A M F L P I M S I I C F V G L L G N G 77

QY 61 M V T A I Y A Y K K O R T K T D V Y I I N L A V A D L L L F T L P F M A V N A V H G W L G K I M C K I T S A L Y T 120
DB 78 L V A L T Y I F E R K L T M D T Y L N L A V A D I L F L T L P F M A Y S A K S W F G V H F C K L I F A I Y K 137

QY 121 I N F V S G M Q F L A C I S I D R Y A V A V T K V P S --- Q S G V K P C W I I C F C V M A A I L I S P O L V E Y 176
DB 138 M S F F S G M L L I C I S I D R Y A I V A Q A V S A H R H R A R V L I S K S C V G I W I A T V L S I P E L L Y S 197

QY 177 T V N D N A --- R C I P F P R Y L G T S M K A L I O M L E I C I G F V P F L I N G V C Y F T A R T L M K P 231
DB 198 D L O R S S E Q A M R C S L I T E H --- V E A F I T I V A Q W I G F L V P L A M S F C Y L V I I R T L L Q A R 254

QY 232 N I K I S R P L K L T V V I V F I V T O L P Y N I V K F C R A I D I I Y S L I T S C M S K M D I A I Q Y T E S I 291
DB 255 N F E R N K A I K I I A V V V I F V F O L P Y N G V L A Q V A N F N I T S T C E L S K O L N I A D V T Y S L 314

QY 292 A L F H S C L N P L Y F E M G A S F K N Y M K V A K K Y G --- S W --- R R O S V E E P F P D 337
DB 315 A C V R C C V N P E L V A F I G V K F R N D L F K L F K D L G C L S Q E Q L R O W S C R H I R S S M S V E --- 369

QY 338 S E G P T E P T S F S 349
DB 370 --- A E T T T F S 377

RESULT 11
US-09-088-337B-15
Sequence 15, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>

```



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; INFORMATION FOR SEQ ID NO: 15
;
; SEQUENCE CHARACTERISTICS:
;
;   LENGTH: 378 amino acids
;
;   TYPE: amino acid
;
;   TOPOLOGY: linear
;
;   MOLECULE TYPE: protein
;
PCT-US93-1153-15

```

Query Match	36.2%;	Score 659;	DB 5;	Length 378;
Best Local Similarity	38.7%;	Pred. No. 5.4e-49;		
Matches 144;	Conservative 66;	Mismatches 124;	Indels 38;	Gaps 7.

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QY      61 MVAIAYYXKORTKTIDYILNLAVADLLFTLPFMAVNAHGVWLGIIMCKITSALYT 120
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QY      121 LNVSGMQLACISIDRYAVATKVS---QSGVGRKPMIICFVMAAILLSIPOLVEY 176
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QY      177 TVWDA-----RCIPFPRYGLGSMKALIQMLEICIGVPEFLIMGVCFYFATRLMKP 231
Db      198 DLQRSSEQAMRCSLTIEH---VEAFITIQAVQWIGTVLEFLMSFCYLIIRTLIQAR 254

QY      232 NIKISRPILKYLTVIVIVITQLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTEST 291
Db      255 NFRNRNAIKIILVVVVVFIVFQLPBYNGVLAQTVANFNITSCTCELKXQNLIAVDVYSL 314

QY      292 ALHNSCLNPLIYFEMASFKYVMKYAKYG-----SN-----RRQRQSYEEPPD 337
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QY      338 SEGTEPTSTFS 349
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RESULT 14
US-08-153-848-7
Sequence 7, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.

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? REISTRATION NUMBER: 35,302
? REFERENCE/DOCKEN NUMBER: 3.1796
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 474-6300
? TELEPHONE: (312) 474-0448
? TELEX: 25-1856
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 410 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-153-848-7

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Query Match	36.2%;	Score 659;	DB 1;	Length 410;
Best Local Similarity	38.7%;	Pred. No. 5.9e-49;		
Matches 144;	Conservative 66;	Mismatches 124;	Indels 38;	Gaps 7

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Db 402 ----ABTTTFS 409

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RESULT 15
 US-09-299-843A-7
 Sequence 7, Application US/09299843A
 Patent No. 6107475
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweikart, Vicki L.
 TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSER: Borum
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/299, 843A
 FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. DHI
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-7

Query Match 36.2%; Score 659; DB 3; Length 410;
Best Local Similarity 38.7%; Pred. No. 5,9e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEONOSTDYVEEENENGTVDYSQYELICKEDYREFAKVFLLPYFLTIVFVIGLAGNS 60
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QY 61 MVAIAIAYKKKORTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITSALT 120
DB 110 LVVLTIVYFRRLKMTMDTYILNLAVADILFLTLFPWYSAKSWVFGVHCKLIFAIYK 169
QY 121 LNFVSGMPLACISIDRYAVATKVS---QSGVGKPCWIIICPCVMMAILISTPOLVY 176
DB 170 MSFSSGMLLLLCISIDRYAVAIQAVSAHRRARVLLISKSCVGIWILATVLSIBELYS 229
QY 177 TVVDNA-----RCIPFPRYLGSMKALIQMLEICIGFVVPFLMGVCYFIFTARTIMKP 231
DB 230 DLQSSSEQAMRCSLITEH---VEAFITIQVAGMVGFLVPLAMSGCYLVIRITLQAR 286
QY 232 NIKISRLKXLTIVIVFIVTQLPNIVKFCRAIDIIYSLITSQNSKRMIDAIQYTESI 291
DB 287 NFERNRAIKYIIIVVVFIVFQLPYNGVLAQTVANFNITSSFCELSKQINIAVDVYSI 346
QY 292 ALFHSCINPLIVFMGASFNQVYMKVAKKYG-----SM-----RRQROSVEEFFPD 337
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QY 338 SEGTEPTSTFS 349
DB 402 ----AETTTFS 409

Search completed: April 13, 2004, 13:19:12
Job time: 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:16:24 ; Search time 46 Seconds
(without alignments)

2000.615 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819
Sequence: 1 MALEQNSTDYEEENMG.....VEEPFDEGPTPTPSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1819	100.0	350	9	US-09-765-994-2
2	1819	100.0	350	9	US-09-796-338A-8
3	1819	100.0	350	10	US-09-968-433-16
4	1819	100.0	350	14	US-10-282-837-8
5	1819	100.0	350	14	US-10-225-567A-607
6	1819	100.0	350	14	US-10-288-222A-10
7	1819	100.0	350	14	US-10-145-566-8
8	1819	100.0	350	14	US-10-239-423-75
9	1819	100.0	350	15	US-10-407-079-84
10	1819	99.7	349	9	US-09-765-994-4
11	1819	99.5	348	12	US-10-403-161-12
12	1819	99.5	350	14	US-10-272-963-22
13	1819	99.5	350	14	US-10-393-807-22
14	1819	99.5	350	15	US-10-417-820A-24
15	1803	99.1	350	10	US-09-910-695-8

16	1620	89.1	350	10	US-09-968-433-79	Sequence 79, Appl
17	1257	69.1	242	14	US-10-073-885-73	Sequence 73, Appl
18	862	47.4	164	12	US-10-276-774-1532	Sequence 1532, Ap
19	761	41.8	175	9	US-09-764-853-584	Sequence 584, App
20	761	41.8	175	10	US-09-989-442-108	Sequence 108, App
21	761	41.8	175	11	US-09-764-886-59	Sequence 59, Appl
22	761	41.8	175	11	US-09-764-875-798	Sequence 798, App
23	761	41.8	175	14	US-10-073-865-91	Sequence 91, Appl
24	761	41.8	175	14	US-10-103-313-382	Sequence 382, App
25	761	41.8	175	14	US-10-073-885-100	Sequence 100, App
26	659	36.2	378	14	US-10-251-385-74	Sequence 74, Appl
27	659	36.2	378	14	US-10-225-567A-68	Sequence 68, Appl
28	659	36.2	378	14	US-10-239-423-70	Sequence 70, Appl
29	659	36.2	378	15	US-10-435-696-48	Sequence 48, Appl
30	659	36.2	475	12	US-10-425-114-56811	Sequence 56811, A
31	655	36.0	378	14	US-10-451-385-204	Sequence 204, App
32	643	35.3	369	14	US-10-239-423-72	Sequence 72, Appl
33	643	35.3	378	14	US-10-164-649-49	Sequence 49, Appl
34	637	35.0	357	9	US-09-903-377-2	Sequence 2, Appl1
35	637	35.0	357	9	US-09-952-385-2	Sequence 2, Appl1
36	637	35.0	357	13	US-09-966-755-2	Sequence 2, Appl1
37	637	35.0	357	13	US-10-000-759A-2	Sequence 2, Appl1
38	637	35.0	357	14	US-10-251-385-24	Sequence 24, Appl
39	637	35.0	357	14	US-10-825-567A-241	Sequence 241, Appl
40	637	35.0	357	14	US-10-239-423-73	Sequence 73, Appl
41	637	35.0	369	11	US-09-826-509-481	Sequence 481, App
42	631	34.7	357	14	US-10-451-385-176	Sequence 176, App
43	605	33.3	367	12	US-10-244-089-2	Sequence 2, Appl1
44	605	33.3	367	14	US-10-254-089-2	Sequence 2, Appl1
45	583	32.1	369	14	US-10-239-423-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-09-765-994-2
Sequence 2, Application US/09765994
Parent No. US20010016336A1
GENERAL INFORMATION:
APPLICANT: ELITS, CATHERINE
TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: GH-70225-C1
CURRENT APPLICATION NUMBER: US/09/765,994
CURRENT FILING DATE: 2001-01-19
PRIORITY APPLICATION NUMBER: 60/055,895
PRIORITY FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: 08/962,922
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-765-994-2

Query Match 100.0%; Score 1819; DB 9; Length 350;
Best Local Similarity 100.0%; Pred. 4.7e-159;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 LNFVSGNQFLACISIDRYAVATVTPSQSGYKPCWIIICPCVMAAILLSIPQLVFYTVND 180
DB 121 LNFVSGNQFLACISIDRYAVATVTPSQSGYKPCWIIICPCVMAAILLSIPQLVFYTVND 180

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Db 241 VLLTVVIVIVTQLPNIVKFCRAIDIIYSLITSCNMRKDIAIQVESIALFHSCLNP 300
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RESULT 2

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US-09-796-338A-8
; Sequence 8, Application US/09796338A
; Patent No. US2002006:522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796,338A
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-338A-8

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Query Match      100.0%; Score 1819; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 4.7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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US-09-968-433-16
; Sequence 16, Application US/09968433
; Patent No. US20030073162A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Yang, Janice
; APPLICANT: Reddy, Koopa
; APPLICANT: Murty, Lynn E.

```

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; APPLICANT: Mathur, Preeti
; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PC-0051 CIP
; CURRENT APPLICATION NUMBER: US/09/968,433
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PERL Program
; SEQ ID NO 16
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073162A1 2547002CD1
US-09-968-433-16

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Query Match      100.0%; Score 1819; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 4.7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

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US-10-282-837-8
; Sequence 8, Application US/10282837
; Patent No. US20030082738A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/10/282,837
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-837-8

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Query Match      100.0%; Score 1819; DB 14; Length 350;
Best Local Similarity 100.0%; Pred. No. 4.7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

US-10-225-567A-607

Sequence 607, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences

APPLICANT: Brown, Joseph P.

APPLICANT: Burner, Glenna C.

APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/257,144

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: PatentIn version 3.1

SEQ ID NO 607

LENGTH: 350

TYPE: PRT

ORGANISM: Homo sapiens

US-10-225-567A-607

Query Match 100.0%; Score 1819; DB 14; Length 350;

Best Local Similarity 100.0%; Pred. No. 4.7e-158;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENNGTYDYSQYELICIKEDYREFAKYFLPVFLTIVFVIGLAGNS 60

Db 1 MALEQNSTDYEEENENNGTYDYSQYELICIKEDYREFAKYFLPVFLTIVFVIGLAGNS 60

QY 61 MVAIAVYKKQRTKTDVYILNLAVADLLFLTPMAVANAHVGLGKIMCKITSALYT 120

Db 61 MVAIAVYKKQRTKTDVYILNLAVADLLFLTPMAVANAHVGLGKIMCKITSALYT 120

QY 121 LNFVSGMQFLACISIDRYAVATVPQSQGVKPCWIIICFCVMAAAILLISIPOLVFYTVND 180

Db 121 LNFVSGMQFLACISIDRYAVATVPQSQGVKPCWIIICFCVMAAAILLISIPOLVFYTVND 180

QY 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

Db 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

QY 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

Db 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

RESULT 6

US-10-288-222A-10

Sequence 10, Application US/10288222A

Publication No. US20030119742A1

GENERAL INFORMATION:

APPLICANT: Logan, Thomas Joseph

APPLICANT: Galvin, Katherine

APPLICANT: Chun, Mayoung

TITLE OF INVENTION: Methods and Compositions to treat

TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 2414,

FILE REFERENCE: M02001-286P(RM)

CURRENT APPLICATION NUMBER: US/10/288,222A

CURRENT FILING DATE: 2002-11-05

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 350

TYPE: PRT

ORGANISM: Homo Sapien

US-10-288-222A-10

Query Match 100.0%; Score 1819; DB 14; Length 350;

Best Local Similarity 100.0%; Pred. No. 4.7e-158;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENNGTYDYSQYELICIKEDYREFAKYFLPVFLTIVFVIGLAGNS 60

Db 1 MALEQNSTDYEEENENNGTYDYSQYELICIKEDYREFAKYFLPVFLTIVFVIGLAGNS 60

QY 61 MVAIAVYKKQRTKTDVYILNLAVADLLFLTPMAVANAHVGLGKIMCKITSALYT 120

Db 61 MVAIAVYKKQRTKTDVYILNLAVADLLFLTPMAVANAHVGLGKIMCKITSALYT 120

QY 121 LNFVSGMQFLACISIDRYAVATVPQSQGVKPCWIIICFCVMAAAILLISIPOLVFYTVND 180

Db 121 LNFVSGMQFLACISIDRYAVATVPQSQGVKPCWIIICFCVMAAAILLISIPOLVFYTVND 180

QY 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

Db 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

QY 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

Db 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

RESULT 7

US-10-145-586-8

Sequence 8, Application US/10145586

Publication No. US20030138690A1

GENERAL INFORMATION:

APPLICANT: Alexandra Glucksmann, Maria

APPLICANT: Silos-Santlago, Immaculada

APPLICANT: M. Galvin, Katherine

APPLICANT: Welch, Nadine

APPLICANT: Curtis, Rory A. J.

APPLICANT: Bandaru, Rajasekhar

APPLICANT: Kapeller-Libermann, Rosana

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS.

TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH

FILE REFERENCE: 10448-188001

CURRENT APPLICATION NUMBER: US/10/145,586

CURRENT FILING DATE: 2002-05-14

Prior Application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 95
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 8
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-586-8

Query Match 100.0%; Score 1819; DB 14; Length 350;
Best Local Similarity 100.0%; Pred. No. 4,7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQONSTDYEEENENGTYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60
DB 1 MLEQONSTDYEEENENGTYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60
QY 61 MVAIAAYKKORTKIDYIILNLAVALDLLLFTLPFWANAVHGVNLGKIMCKITSALT 120
DB 61 MVAIAAYKKORTKIDYIILNLAVALDLLLFTLPFWANAVHGVNLGKIMCKITSALT 120
QY 121 LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICVWMAAILLSIPOLVFYTVND 180
DB 121 LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICVWMAAILLSIPOLVFYTVND 180
QY 181 NARCIPIPRVLTGSMKALIQMLEICIGFVPEFLMGVCYFTARTLMKMPNIXSRPLK 240
DB 181 NARCIPIPRVLTGSMKALIQMLEICIGFVPEFLMGVCYFTARTLMKMPNIXSRPLK 240
QY 241 VLLTVIVIVITQLPNIYKFCRAIDIIYSLITSCMSKRMIDIAQVTSIALFHSCLNP 300
DB 241 VLLTVIVIVITQLPNIYKFCRAIDIIYSLITSCMSKRMIDIAQVTSIALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKAKYGSWROROSVEEFPDSEGTPEPTSTFSI 350
DB 301 ILVFMGASFKNYVMKAKYGSWROROSVEEFPDSEGTPEPTSTFSI 350

RESULT 8

US-10-239-423-75
Sequence 75, Application US/10239423
Publication No. US20030186889A1
GENERAL INFORMATION:
APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ABERMANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SODSBERG, Nikolaaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217Us
CURRENT APPLICATION NUMBER: US/10/239,423
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 75
LENGTH: 350
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-75

Query Match 100.0%; Score 1819; DB 14; Length 350;
Best Local Similarity 100.0%; Pred. No. 4,7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQONSTDYEEENENGTYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60
DB 1 MLEQONSTDYEEENENGTYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60

QY 61 MVAIAAYKKORTKIDYIILNLAVALDLLLFTLPFWANAVHGVNLGKIMCKITSALT 120
DB 61 MVAIAAYKKORTKIDYIILNLAVALDLLLFTLPFWANAVHGVNLGKIMCKITSALT 120
QY 121 LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICVWMAAILLSIPOLVFYTVND 180
DB 121 LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICVWMAAILLSIPOLVFYTVND 180
QY 181 NARCIPIPRVLTGSMKALIQMLEICIGFVPEFLMGVCYFTARTLMKMPNIXSRPLK 240
DB 181 NARCIPIPRVLTGSMKALIQMLEICIGFVPEFLMGVCYFTARTLMKMPNIXSRPLK 240
QY 241 VLLTVIVIVITQLPNIYKFCRAIDIIYSLITSCMSKRMIDIAQVTSIALFHSCLNP 300
DB 241 VLLTVIVIVITQLPNIYKFCRAIDIIYSLITSCMSKRMIDIAQVTSIALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKAKYGSWROROSVEEFPDSEGTPEPTSTFSI 350
DB 301 ILVFMGASFKNYVMKAKYGSWROROSVEEFPDSEGTPEPTSTFSI 350

RESULT 9

US-10-407-079-84
Sequence 84, Application US/10407079
Publication No. US20030215860A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Siles-Santiago, Immaculada
APPLICANT: Carroll, Joseph M.
APPLICANT: Galvin, Katherine M.
TITLE OF INVENTION: 18636, 2466, 43238, 1983, 52881, 2398,
TITLE OF INVENTION: 45449, 59289, 52872 AND 26908 MOLECULES AND USES THEREFOR
FILE REFERENCE: M103-0510NM
CURRENT APPLICATION NUMBER: US/10/407,079
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 10/226,102
PRIOR FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,041
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 10/225,094
PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/314,185
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 10/272,417
PRIOR FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/715,790
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 60/191,845
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 10/282,837
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 09/796,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186,059
PRIOR FILING DATE: 2000-02-29
REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 84
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-10-407-079-84

Query Match 100.0%; Score 1819; DB 15; Length 350;
Best Local Similarity 100.0%; Pred. No. 4,7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQONSTDYEEENENGTYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60
DB 1 MLEQONSTDYEEENENGTYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60

QY 61 MVAIAYKKORTKTDVYIILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 120
 DB 61 MVAIAYKKORTKTDVYIILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILLSIPOLVFYTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILLSIPOLVFYTVND 180
 QY 181 NARCIPFPRLYGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMMPNIXSRPLK 240
 DB 181 NARCIPFPRLYGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMMPNIXSRPLK 240
 QY 241 VLLTVVIVEIVTQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAQVTSIALFHSCLNIP 300
 DB 241 VLLTVVIVEIVTQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAQVTSIALFHSCLNIP 300
 QY 301 LTVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350
 DB 301 LTVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

RESULT 10

US-09-765-994-4
 ; Sequence 4, Application US/09765994
 ; Patent No. US20010016336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ELLIS, CATHERINE
 ; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: GH-70225-C1 (HEIAC41)
 ; CURRENT APPLICATION NUMBER: US/09/765,994
 ; PRIOR FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: 60/055,895
 ; PRIOR FILING DATE: 1997-08-15
 ; PRIOR APPLICATION NUMBER: 08/962,922
 ; PRIOR FILING DATE: 1997-10-27
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 349
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-765-994-4

Query Match 99.7%; Score 1814; DB 9; Length 349;

Best Local Similarity 100.0%; Pred. No. 1.4e-157; Mismatches 0; Indels 0; Gaps 0;

Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEQNSTDYEEENENGTVDYSQYELICIKEDVREFAKVFLPVFLTIIVFVIGLAGNSM 61
 DB 1 ALEQNSTDYEEENENGTVDYSQYELICIKEDVREFAKVFLPVFLTIIVFVIGLAGNSM 60
 QY 62 VVAIAYKKORTKTDVYIILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 121
 DB 61 VVAIAYKKORTKTDVYIILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 120
 QY 122 NFNVSQMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILLSIPOLVFYTVND 181
 DB 122 NFNVSQMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILLSIPOLVFYTVND 180
 QY 182 ARCIPIFPRLYGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMMPNIXSRPLK 241
 DB 181 ARCIPIFPRLYGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMMPNIXSRPLK 240
 QY 242 LTVVIVIVEIVTQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAQVTSIALFHSCLNIP 301
 DB 241 LTVVIVIVEIVTQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAQVTSIALFHSCLNIP 300
 QY 302 LTVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350
 DB 301 LTVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 349

RESULT 11
 US-10-403-161-12
 ; Sequence 12, Application US/10403161
 ; Publication No. US20040043930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, David et al.
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-573C
 ; CURRENT APPLICATION NUMBER: US/10/403,161
 ; PRIOR FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: 60/370349
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: 60/384543
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: 60/370969
 ; PRIOR FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: 60/403748
 ; PRIOR FILING DATE: 2002-08-15
 ; PRIOR APPLICATION NUMBER: 60/372019
 ; PRIOR FILING DATE: 2002-04-12
 ; PRIOR APPLICATION NUMBER: 60/374379
 ; PRIOR FILING DATE: 2002-04-22
 ; PRIOR APPLICATION NUMBER: 09/779679
 ; PRIOR FILING DATE: 2001-02-08
 ; PRIOR APPLICATION NUMBER: 60/161045
 ; PRIOR FILING DATE: 2000-02-08
 ; PRIOR APPLICATION NUMBER: 10/055877
 ; PRIOR FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: 60/262892
 ; PRIOR FILING DATE: 2001-01-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 173
 ; SOFTWARE: Cnaseqdist version 0.1
 ; SEQ ID NO 12
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-403-161-12

Query Match 99.5%; Score 1810; DB 12; Length 348;

Best Local Similarity 100.0%; Pred. No. 3.1e-157; Mismatches 0; Indels 0; Gaps 0;

Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LEQNSTDYEEENENGTVDYSQYELICIKEDVREFAKVFLPVFLTIIVFVIGLAGNSM 62
 DB 1 LEQNSTDYEEENENGTVDYSQYELICIKEDVREFAKVFLPVFLTIIVFVIGLAGNSM 60
 QY 63 VVAIAYKKORTKTDVYIILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 122
 DB 61 VVAIAYKKORTKTDVYIILNLAVALDLLFTLPFAVNAVHGVLGKIMCKITSALYT 120
 QY 123 FVSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILLSIPOLVFYTVND 182
 DB 121 FVSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILLSIPOLVFYTVND 180
 QY 183 RCIPFPRLYGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMMPNIXSRPLK 242
 DB 181 RCIPFPRLYGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMMPNIXSRPLK 240
 QY 243 LTVVIVIVEIVTQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAQVTSIALFHSCLNIP 302
 DB 241 LTVVIVIVEIVTQLPYNIVKFCRAIDIIYSLITSCKMSKRMIDIAQVTSIALFHSCLNIP 300
 QY 303 YVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350
 DB 301 YVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 348

RESULT 12

US-10-272-983-22
 ; Sequence 22, Application US/10272983
 ; Publication No. US20030148450A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 22
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-22

Query Match      99.5%; Score 1810; DB 14; Length 350;
Best Local Similarity 99.4%; Pred. No. 3.2e-157;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 M A L E O N O S T D Y Y E E N E N G T D Y S Q Y E L I C I K E D Y R E F A K V L P F L T I V F I G L A G N S 60
DB 1 M A L E O N O S T D Y Y E E N E N G T D Y S Q Y E L I C I K E D Y R E F A K V L P F L T I V F I G L A G N S 60
QY 61 M V A I A Y Y K K O R T K D V Y I L N L A V A D L L L F T L P F M A V A N A H G W L G K I M C K I T S A L Y T 120
DB 61 M V A I A Y Y K K O R T K D V Y I L N L A V A D L L L F T L P F M A V A N A H G W L G K I M C K I T S A L Y T 120
QY 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C F C V M M A A I L L S I P O L V F Y T V N D 180
DB 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C F C V M M A A I L L S I P O L V F Y T V N D 180
QY 181 N A R C I P F P R Y L G T S M K A L I Q M L E I C I G F V P F L I N G V C Y F I T A R T L M K M P I K I S R P L K 240
DB 181 N A R C I P F P R Y L G T S M K A L I Q M L E I C I G F V P F L I N G V C Y F I T A R T L M K M P I K I S R P L K 240
QY 241 V L L T V I V F I V T Q L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I A L F H S C L N P 300
DB 241 V L L T V I V F I V T Q L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I A L F H S C L N P 300
QY 301 I L V F M G A S F K N Y V M V A K K Y G S M R R O S V E E F P D S E G P T E P T S F S I 350
DB 301 I L V F M G A S F K N Y V M V A K K Y G S M R R O S V E E F P D S E G P T E P T S F S I 350

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RESULT 13
US-10-393-807-22
; Sequence 22, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.

```

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; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 22
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-807-22

Query Match      99.5%; Score 1810; DB 14; Length 350;
Best Local Similarity 99.4%; Pred. No. 3.2e-157;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 M A L E O N O S T D Y Y E E N E N G T D Y S Q Y E L I C I K E D Y R E F A K V L P F L T I V F I G L A G N S 60
DB 1 M A L E O N O S T D Y Y E E N E N G T D Y S Q Y E L I C I K E D Y R E F A K V L P F L T I V F I G L A G N S 60
QY 61 M V A I A Y Y K K O R T K D V Y I L N L A V A D L L L F T L P F M A V A N A H G W L G K I M C K I T S A L Y T 120
DB 61 M V A I A Y Y K K O R T K D V Y I L N L A V A D L L L F T L P F M A V A N A H G W L G K I M C K I T S A L Y T 120
QY 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C F C V M M A A I L L S I P O L V F Y T V N D 180
DB 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C F C V M M A A I L L S I P O L V F Y T V N D 180
QY 181 N A R C I P F P R Y L G T S M K A L I Q M L E I C I G F V P F L I N G V C Y F I T A R T L M K M P I K I S R P L K 240
DB 181 N A R C I P F P R Y L G T S M K A L I Q M L E I C I G F V P F L I N G V C Y F I T A R T L M K M P I K I S R P L K 240
QY 241 V L L T V I V F I V T Q L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I A L F H S C L N P 300
DB 241 V L L T V I V F I V T Q L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I A L F H S C L N P 300
QY 301 I L V F M G A S F K N Y V M V A K K Y G S M R R O S V E E F P D S E G P T E P T S F S I 350
DB 301 I L V F M G A S F K N Y V M V A K K Y G S M R R O S V E E F P D S E G P T E P T S F S I 350

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RESULT 14
US-10-417-820A-24
; Sequence 24, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.

```

APPLICANT: Behan, Dominic P.
 TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
 FILE REFERENCE: 7:US28,CON
 CURRENT APPLICATION NUMBER: US/10/417,820A
 PRIOR FILING DATE: 2003-04-16
 PRIOR APPLICATION NUMBER: 09/416,760
 PRIOR FILING DATE: 1999-10-12
 PRIOR APPLICATION NUMBER: 09/170,496
 PRIOR FILING DATE: 1998-10-13
 PRIOR APPLICATION NUMBER: 60/110,060
 PRIOR FILING DATE: 1998-11-27
 PRIOR APPLICATION NUMBER: 60/120,416
 PRIOR FILING DATE: 1999-02-16
 PRIOR APPLICATION NUMBER: 60/121,852
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/109,213
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: 60/123,944
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,945
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,948
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,951
 PRIOR FILING DATE: 1999-03-12
 Remaining Prior Application data removed - See file Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 155
 SOFTWARE: Patent version 3.2
 SEQ ID NO: 24
 LENGTH: 350
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-417-820A-24

Query Match 99.5%; Score 1810; DB 15; Length 350;
 Best Local Similarity 99.4%; Pred. No. 3.2e-157;
 Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENNGTYDSQYELICIKEDVREFAKFLPVFLTIYFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENENNGTYDSQYELICIKEDVREFAKFLPVFLTIYFVIGLAGNS 60
 QY 61 MVVAIVAYVKKORTKIDVYILNLAVADLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
 DB 61 MVVAIVAYVKKORTKIDVYILNLAVADLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATVPQSOGVGRPCWIIICFCVMAAILLSIPOLVFYTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATVPQSOGVGRPCWIIICFCVMAAILLSIPOLVFYTVND 180
 QY 181 NARCIIFPRYLGSMKALIQMLEICIGFVFPFLMGVCYFITARLTMKPNKISRLPK 240
 DB 181 NARCIIFPRYLGSMKALIQMLEICIGFVFPFLMGVCYFITARLTMKPNKISRLPK 240
 QY 241 VLLTVIVFIVTQLPNIYVFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300
 DB 241 VLLTVIVFIVTQLPNIYVFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300
 QY 301 ILVYFMGASFKNYVMKAKKYGSROROSVEEFPDSEPTSTSTFSI 350
 DB 301 ILVYFMGASFKNYVMKAKKYGSROROSVEEFPDSEPTSTSTFSI 350

RESULT 15
 US-09-910-695-8
 Sequence 8, Application US/09910695
 Publication No. US20030166052A1
 GENERAL INFORMATION:
 APPLICANT: Hedrick, Joseph A.
 Vicari, Alain P.
 Zlocnik, Albert
 TITLE OF INVENTION: Mammalian Chemokines; Receptors;

Reagents; Uses
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/910,695
 FILING DATE: 20-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/122,585
 FILING DATE: 24-Jul-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0757
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 852-9196
 TELEFAX: (650) 496-1200
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-910-695-8

Query Match 99.1%; Score 1803; DB 10; Length 350;
 Best Local Similarity 99.4%; Pred. No. 1.4e-156;
 Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENNGTYDSQYELICIKEDVREFAKFLPVFLTIYFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENENNGTYDSQYELICIKEDVREFAKFLPVFLTIYFVIGLAGNS 60
 QY 61 MVVAIVAYVKKORTKIDVYILNLAVADLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
 DB 61 MVVAIVAYVKKORTKIDVYILNLAVADLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATVPQSOGVGRPCWIIICFCVMAAILLSIPOLVFYTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATVPQSOGVGRPCWIIICFCVMAAILLSIPOLVFYTVND 180
 QY 181 NARCIIFPRYLGSMKALIQMLEICIGFVFPFLMGVCYFITARLTMKPNKISRLPK 240
 DB 181 NARCIIFPRYLGSMKALIQMLEICIGFVFPFLMGVCYFITARLTMKPNKISRLPK 240
 QY 241 VLLTVIVFIVTQLPNIYVFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300
 DB 241 VLLTVIVFIVTQLPNIYVFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300
 QY 301 ILVYFMGASFKNYVMKAKKYGSROROSVEEFPDSEPTSTSTFSI 350
 DB 301 ILVYFMGASFKNYVMKAKKYGSROROSVEEFPDSEPTSTSTFSI 350

Search completed: April 13, 2004, 13:20:10
 Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:19 ; Search time 20 Seconds
(without alignments)
1683.352 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819
Sequence: 1 MALEONQSTDYEEENMNG.....VEEFPDSEGPTEPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 781.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	1620	89.1	350 2 JN0621	G protein-coupled
2	659	36.2	378 2 B55735	lymphocyte-specific
3	650	35.7	378 2 A55735	G protein-coupled
4	643	35.3	378 2 A55735	G protein-coupled
5	583	32.1	369 2 UC5068	G protein-coupled
6	537.5	29.5	360 2 A57160	chemokine (C-C) re
7	534.5	29.4	360 2 A57160	interleukin-8 rece
8	524	28.8	354 2 I58186	probable G protein
9	522.5	28.7	355 2 UC4304	orphan G protein-c
10	522.5	28.7	360 2 UC4587	chemokine (C-C) re
11	518.5	28.5	354 2 B55735	G protein-coupled
12	511	28.1	358 2 A53752	interleukin-8 rece
13	501.5	27.6	355 2 UC1231	interleukin-8 rece
14	500.5	27.5	352 2 A45747	neuropeptide Y/pep
15	499.5	27.5	353 2 S28787	neuropeptide Y/pep
16	493.5	27.1	352 2 G00048	fusin (LESTRA) - C
17	492	27.0	360 2 UC2443	chemokine (C-C) re
18	489.5	26.9	350 2 A39445	interleukin-8 rece
19	486	26.7	355 2 UC5067	G protein-coupled
20	485	26.7	355 2 A39339	macrophage inflamm
21	484.5	26.6	352 2 A43113	chemokine (C-C) re
22	483.5	26.6	359 2 A48921	interleukin-8 rece
23	482	26.5	374 2 I38450	chemokine (C-C) re
24	479.5	26.4	359 2 I49341	MMP-1 alpha recept
25	476.5	26.2	367 2 A50349	interleukin-inducib
26	474	26.1	355 2 A45177	chemokine (C-C) re
27	471	25.9	356 2 S42056	interleukin-8 rece
28	470	25.8	383 2 S55594	G protein-coupled
29	461.5	25.4	355 2 G02436	chemokine (C-C) re

ALIGNMENTS

RESULT 1

JN0621
G protein-coupled receptor type B - bovine

C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000

C/Accession: JN0621
R/Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

A/Title: Identification of novel members of G-protein coupled receptor superfamily expres
A/Reference number: JN0621; MUID:93326166; PMID:8392843

A/Accession: JN0621
A/Molecule type: mRNA

A/Residues: 1-350 <MRA>
A/Cross-References: GB:863848; NID:9399710; PIDN:A4827547.1; PID:9399711

A/Experimental source: tongue taste papillae
C/Comment: This protein is involved in modulating taste sensitivity or regeneration of te

C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F/42-66/Domain: transmembrane #status predicted <TM2>
F/80-99/Domain: transmembrane #status predicted <TM3>
F/114-135/Domain: transmembrane #status predicted <TM4>
F/154-175/Domain: transmembrane #status predicted <TM5>
F/200-222/Domain: transmembrane #status predicted <TM6>
F/242-265/Domain: transmembrane #status predicted <TM7>
F/284-306/Domain: transmembrane #status predicted <TM7>
F/6,19/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 89.1% Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.4e-131;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY	1	MALEONQSTDYEEENMNGTGYDQYELICKEQVREFAKFLVPTTIVFVIGLAGNS	60
DB	1	MAVEYKQSTDYEEENMNDTHDYSQYEVICKEVRFKFLPAFTTIAFIILAAGNS	60
QY	61	MYVAIYAYKKQRTKTDVYIINLAVADLLFTLPFAVNAVHGVNLGKIKITSAIYT	120
DB	61	TVAIYAYKKRRTKTDVYIINLAVADLLFTLPFAVNAVHGVNLGKIKITSAIYT	120
QY	121	LMFVSGMGLACISIDRYAAVTKVPSQSGVGRKCIIFECVMAAIIISIPOLVFTYND	180
DB	121	VAFVSGMGLACISIDRYAAVTKVPSQSGVGRKCIIFECVMAAIIISIPOLVFTYND	180
QY	181	NARCIPFPFVYLGTSKMLIQMLEICIGFVPEFLIMGVCYFTTAPTKMKNIKISRLK	240
DB	181	KARCIPFPFVYLGTSKMLIQMLEICIGFVPEFLIMGVCYFTTAPTKMKNIKISRLK	240
QY	241	VLLTVIVIVITVQLPYNIVKFCRAIDITYSITSCMKRMKMDIAOVESIALPFSCLNP	300
DB	241	VLLTVIVIVITVQLPYNIVKFCRAIDITYSITSCMKRMKMDIAOVESIALPFSCLNP	300
QY	301	ILVFWGSAFKNYVWKVAKYGSNRRORSVEEFPDSEGPTEPTSTFSI 350	

Db 301 VLVFVNGTSPKRYIMVAKKYGSRQRQVNERIPESDEDAIEPTSTFBI 350

RESULT 2

lymphocyte-specific G protein-coupled receptor EB11 - human
B55735

N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C:Species: Homo sapiens (man)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000

C:Accession: B55735; S52443

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: B55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31581; NID:G468319; PIDN:AAA74231.1; PID:G468320

R:Burghalter, R.; Kempkes, B.; Staebler, K.; Lipp, M. Submitted to the EMBL Data Library, February 1995

A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans

A:Reference number: S52443

A:Accession: S52443

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 21-378 <BUR>

A:Cross-references: EMBL:X84702

C:Genetics:

A:Gene: GDB:CMK87; EB11; BLR2; CCR7

A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 36.2%; Score 659; DB 2; Length 378;

Best Local Similarity 38.7%; Pred. No. 4.9e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSTDYVEENENMGTYDYSQYELICIKEDVREPAKVLPEVLTIVFVIGLAGNS 60

Db 21 VCLCQDEVTDDYIGDNT---TVDTYLFESLCKSKDVRNFKAMFLPMYSVLCFVGLGNG 77

QY 61 MVAIAYKKKRTKDVYILNLAVADLLFTLPFMANAVHGVLGKIMKISALYT 120

Db 78 LVVLTYIFPRKIMTDYILNLAVADLLFTLPFMAISAASWVGVHPCKLIFATYK 137

QY 121 LNFVSGMQLACTSIDRYVAATKPS---QSGVGKPCWIIQCVMAAILLSIPOLVY 176

Db 138 MSFSGMLLLCTSIDRYVAIVQAVSAHRHARVLLISKLSGVGIWILATVLSIPELYS 197

QY 177 TVNDNA-----RCIPFPRVLGSMKALLQMEICIGFVPPFLIMGVCFITARTLMKP 231

Db 198 DLRSSSEQMRQSLTHER--VEAFITTVQAVMVGFLVPLAMSFVCLVIRTLQAR 254

QY 232 NIKISPELKYLTIVVIFVITQLPYNIYKFCRAIDIIYSLITSNNKSKMDIAIQTESI 291

Db 255 NPEKNKAIKIIVAVVVFIVFQLPYNGVLAQTVANFNITSSCELSKQLNTIAYDTYSL 314

QY 292 ALHSCINPLIYFMGASFKNYMKYAKKYG-----SW-----RQROSVVEFPD 337

Db 315 ACVRCNCPFLYAFIVGKFRNDLFLKFDGLCSQSLQWSSCRHIRSSMSVE----- 369

QY 338 SEGPTEPTSTFS 349

Db 370 ----AETTTFS 377

RESULT 3

G protein-coupled receptor EB11 - mouse

A55735

C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999

C:Accession: A55735

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: A55735

A:Status: preliminary

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999

C:Accession: A55735

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: A55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31580; NID:G468340; PIDN:AAA74232.1; PID:G468341

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 35.7%; Score 650; DB 2; Length 378;

Best Local Similarity 38.3%; Pred. No. 2.9e-48;

Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

QY 5 QNSTDYVEENENMGTYDYSQYELICIKEDVREPAKVLPEVLTIVFVIGLAGNSVVA 64

Db 25 QDEVTDDYIGDNT---TVDTYLFESLCKSKDVRNFKAMFLPMYSVLCFVGLGNGVLIL 81

QY 65 IYAYKKKRTKDVYILNLAVADLLFTLPFMANAVHGVLGKIMKISALYTINLV 124

Db 82 TYIFPRKIMTDYILNLAVADLLFTLPFMAISAASWVGVHPCKLIFATYKLSF 141

QY 125 SGMQFLACTSIDRYVAATKPSQSG-----VGRPCWIIQCVMAAILLSIPOLVYT 177

Db 142 SGMILLCTSIDRYVAIVQAVSAHRHARVLLISK--LSCVGIWILATVLSIPELYS 198

QY 178 VNDA-----RCIPFPRVLGSMKALLQMEICIGFVPPFLIMGVCFITARTLMKP 230

Db 199 LQNSGDETLKQ---SLVSAQVEALITTVQAVMVGFLVPLAMSFVCLVIRTLQAR 253

QY 231 NIKISPELKYLTIVVIFVITQLPYNIYKFCRAIDIIYSLITSNNKSKMDIAIQTES 290

Db 254 NPEKNKAIKIIVAVVVFIVFQLPYNGVLAQTVANFNITSSCELSKQLNTIAYDTYS 313

QY 291 IALHSCINPLIYFMGASFKNYMKYAKKYGSRNR-----QGVVEFPDSEPT 343

Db 314 LASVRCNCPFLYAFIVGKFRNDLFLKFDGLCSQSLQWSSCRHIRSSMSVMB--AE 371

QY 344 PTSTFS 349

Db 372 TTTTFS 377

RESULT 4

A55680

G protein-coupled peptide receptor EB1 1 - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C:Accession: A45680

R:Bitkenbach, M.; Josefsen, K.; Valamanchili, R.; Lenoir, G.; Kieff, E. J. Virol. 67, 2209-2220, 1993

A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p

A:Reference number: A45680; MUID:91181173; PMID:8353238

A:Accession: A45680

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-378 <BIR>

A:Cross-references: GB:L08176; NID:G183484; PID:G183485

A:Experimental source: B-lymphocytes

A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:127095)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 35.3%; Score 643; DB 2; Length 378;

Best Local Similarity 39.0%; Pred. No. 1.2e-47;

Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

QY 1 MALEQNSTDYVEENENMGTYDYSQYELICIKEDVREPAKVLPEVLTIVFVIGLAGNS 60

Db 21 VCLCQDEVTDDYIGDNT---TVDTYLFESLCKSKDVRNFKAMFLPMYSVLCFVGLGNG 77

QY 61 MVAIAYKKKRTKDVYILNLAVADLLFTLPFMANAVHGVLGKIMKISALYT 120

Db 78 LVVLTYIFPRKIMTDYILNLAVADLLFTLPFMAISAASWVGVHPCKLIFATYK 137

QY 121 LNFVSGMQLACTSIDRYVAATKPS---QSGVGKPCWIIQCVMAAILLSIPOLVY 176

Db 138 MSFSGMLLLCTSIDRYVAIVQAVSAHRHARVLLISKLSGVGIWILATVLSIPELYS 197

QY 177 TVNDNA-----RCIPFPRVLGSMKALLQMEICIGFVPPFLIMGVCFITARTLMKP 231

Db 198 DLRSSSEQMRQSLTHER--VEAFITTVQAVMVGFLVPLAMSFVCLVIRTLQAR 254

Db 21 VCLQCEVTDYDYGNT---TVDTLTFESLCKKDVNFKAMFLPMISIIICFVGLGNG 77
Qy 61 MVAIAIYAYKQRTKTVTLINLAVALDLFLFLPFMAVANAAGWLGIKMKITSAIYT 120
Db 78 LVLVLTITVFRLKTMVDYTLINLAVALDLFLFLPFMAVANAAGWLGIKMKITSAIYT 137
Qy 121 LNVVSGMPLACISIDRYAVATKVPSSQGVKPCMI--CFCYMAA--ALLISIPOLVY 176
Db 138 MSFSSGKLLLLCISIDRYAVATKVPSSQGVKPCMI--CFCYMAA--ALLISIPOLVY 197
Qy 177 TVNDNA-----RCIPFPRYLGTSMKALITOMLEICIGFVFPFLMGVCYFIARTLMKAP 231
Db 198 DLGRSSSEQAMRCSLIEH---VEAFITIOVAGWGLFVPLLMASFCLVLIIRILQAR 254
Qy 232 NITISRLKLVLTIVVITVITQLPYINVKFCRAIDIIYISITSCNMSKMDIAIQVTEI 291
Db 255 NFRNKAIKIVIAVVVVFIVFOLPYNQVLAQTVANFNITSTYCELSKQNTAYDTYSL 314
Qy 292 ALFHSCNPLIYFMGASFKNYVMKAKKYG-----SM-----RROQSVSEFPED 337
Db 315 ACVRCNPLIYAFIGKFRNDLFLKFDGLCSQSLQKQMSCHIRRSMSVE----- 369
Qy 338 SEGPTEPTSTFS 349
Db 370 ----AETTTTFS 377

RESULT 5

UCS068
G:Protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #ext_change 21-Jul-2000
C/Accession: JCS068
R:Zaballo, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A>Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G
A/Reference number: JCS067, MUID:97040707, PMID:8886020
A/Accession: JCS068
A/Molecule type: DNA
A/Residues: 1-369 <ZAB>
A/Cross-references: EMBL:Z79784, NID:g1668737, PIRN:CA802144.1, PID:g1668738
C/Comment: This protein belongs to the family of alpha chemokine receptors.
C/Genetics:
A:Gene: GGB:CKMR6, STRL22, GPR29, CCR6, CKR-L3, GPR-CY4
A:Cross-references: GDB:5370639, OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-66/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 32.1%; Score 583; DB 2; Length 369;
Best Local Similarity 36.1%; Pred. No. 1,6e-42;
Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;

Qy 8 STDYVEENMGNGYDYSQYELICIKEDVREPAKVFPLTIVFVIGLAGNSMVAIYAY 67
Db 18 NTSIYSVDSSE-----LCSLOEVARQFSRLVPIYSICVFGLLGNLIVITTA 67
Qy 68 YXXKQRTKTVTLINLAVALDLFLFLPFMAVANAAGWLGIKMKITSAIYTINLVSG 126
Db 68 FYKARSMETVYTLINLAVALDLFLFLPFMAVANAAGWLGIKMKITSAIYTINLVSG 127
Qy 127 MQLVACISIDRYAVATKVPSSQGVKPCMI--CFCYMAA--ALLISIPOLVY---YTUN 179
Db 128 MLVLTITCISIDRYAVATKVPSSQGVKPCMI--CFCYMAA--ALLISIPOLVY---YTUN 187
Qy 180 DNACIPFPRYLGTSMKALITOMLEICIGFVFPFLMGVCYFIARTLMKAPENIKI 235

Db 188 GSDVC---EPKQGVSEIRKMLMGLLELFGFIFLMFIFCYTPIKTLVQAQNSKR 244
Qy 236 SRPLKLVLTIVVITVITQLPYINVKFCRAIDIIYISITSCNMSKMDIAIQVTEI 295
Db 245 HKARVIAVAVLVAQIQPHNWVLVTAAN-LGRKARSQSESLIGYTKVTVLAFH 303
Qy 296 SCNLPILYFMGASFKNYVMKAKKYGSMRROQS 330
Db 304 CCLNPVLAFTIGQFRNYFLKILDLWCVRKYS 338

RESULT 6

AS7160
Chemokine (C-C) receptor 4 - human
N/Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #ext_change 21-Jul-2000
C/Accession: AS7160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; We
J. Biol. Chem. 270, 19495-19500, 1995
A>Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDN
A/Reference number: AS7160, MUID:95370289, PMID:7642634
A/Accession: AS7160
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-360 <POW>
A/Cross-references: GB:X85740, NID:g1370103, PIRN:CA85743.1, PID:g9571452
A/Note: source clone K5-5
C/Genetics:
A:Gene: GDB:CKMR4
A/Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276,110-187/Disulfide bonds: #status predicted
F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 29.5%; Score 537.5; DB 2; Length 360;
Best Local Similarity 35.8%; Pred. No. 1.3e-38;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

Qy 10 DYVEENMGNGYDYSQYELICIKEDVREPAKVFPLTIVFVIGLAGNSMVAIYAY 69
Db 8 DTLDESISNVYIYES-PRKCTKEGKAFGLFLPLYSIVFVFGLLGNVVLVLFKY 67
Qy 70 KKQRTKTVTLINLAVALDLFLFLPFMAVANAAGWLGIKMKITSAIYTINLVSGQGF 129
Db 68 KRLRMTVYTLINLAVALDLFLFLPFMAVANAAGWLGIKMKITSAIYTINLVSGQGF 127
Qy 130 LACISIDRYAVATKVPSSQGVKPCMI--CFCYMAA--ALLISIPOLVY---YTUN 179
Db 128 VMLMSIDRYAVATKVPSSQGVKPCMI--CFCYMAA--ALLISIPOLVY---YTUN 182
Qy 180 DNACIPFPRYLGTSMKALITOMLEICIGFVFPFLMGVCYFIARTLMKAPENIKI 238
Db 183 NHTYKITYS--INSTWKVSSLEINILGIVPLGIMLFCYSWIRTLQCKNEKXKA 240
Qy 239 LKVLTVIVFVITQLPYINVKFCRAIDIIYISITSCNMSKMDIAIQVTEI 298
Db 241 VKMIAVAVLVAQIQPHNWVLVTAAN-LGRKARSQSESLIGYTKVTVLAFH 303
Qy 299 NPLIYFMGASFKNYVMKAKKYGSMRROQS 330

DB 300 NPIIYFLEGEKFKYIILQLFK 320

RESULT 7

AS53611

Interleukin-8 receptor type B - human

C/Species: Homo sapiens (man)

C/Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999

C/Accession: I37898; 138712; AS3611; A39446

R/Author: S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 269, 26381-26389, 1994

A/Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type B

A/Reference number: 137898; PMID:95014476; PMID:7923358

A/Accession: I37898

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-360 <RES>

A/Cross-references: EMBL:U11869; NID:G511801; PIDN:AA60656.1; *PID:G511803

A/Accession: I38712

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-15 <RES>

A/Cross-references: EMBL:U11872; NID:G511808; PIDN:AAA6380.1; PID:G511809; EMBL:U11873; 11876; NID:G511816; PID:G511817; EMBL:U11877; NID:G511818; PID:G511819; EMBL:U11878; NID:R/Sprienger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelyin, D.J.

J. Biol. Chem. 269, 11065-11072, 1994

A/Title: Structure, genomic organization, and expression of the human interleukin-8 receptor

A/Reference number: A53611; PMID:94209273; PMID:7512557

A/Accession: A53611

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 6-360 <SPR>

A/Cross-references: GB:M99412; GB:L19593

R/Murphy, P.M.; Tiffany, H.L.

Science 253, 1280-1283, 1991

A/Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor

A/Reference number: A39446; PMID:91368200; PMID:1891716

A/Accession: A39446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 6-360 <MR>

A/Cross-references: GB:M73969

C/Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, in

C/Genetics: GDB:IL8RA; IL8RA

A/Accession: GDB:IL8RA

A/Cross-references: GDB:127866; OMIM:146928

A/Map position: 2q35-2q35

C/Superfamily: Vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.4%; Score 534.5; DB 2; Length 360;

Best Local Similarity 33.2%; Pred. No. 2.3e-38;

Matches 120; Conservative 75; Mismatches 141; Indels 25; Gaps 8;

3 LEONOSTDYVENENNGYDYSOYELI-----CIKEDYREPAKVFLLPFLTVIVEVIGLA 57

6 MEDSDPEDFMKGDDLSYSGSTLPPFLDAPCPBPESL-EINKYFVITVIALVFLSL 64

58 GNSMVAIAIYKXKTKTDVYILNIAVADLLFLPMAVNAVHGWLTGKIMKITS 117

65 GNSLVMLVLLISVSGSVTDVYLLNLADLLFALLPMAASKVNGWTFGLCKVSL 124

118 LYLINFSVGMQFLACISIDRYAV--TKVPSQSGVGRKPCWIIICVMAAAILSPOLV 174

125 LKENVYSGILLACISVDRIATVATRTIQKRY--LVKFCISIWGLSHLLAPVIL 182

175 F---YTVNDNACITFRFYIG--TSKALIQMLEIGISVFPILMGVCFITATL 227

183 FRRITVSSNVSPACY---EDMGNTANRMLRLIPSGFIVPLILMLFCYGGTFLTL 238

228 MKAPNIKISRLKVLTVIVFIVTOLPYNIVFCRAIDIIISLITSCNMSKMDIAIOV 287

DB 239 FKAMGQKRAHMEVIRAVVILFLLCWLFPYNVLLADTLARTQYIGETCERRRHIDRALDA 298

QY 288 TESIALFHSCLNPLIVFENGASFKYVMKYAKYSGSRQ---RQVESEFPDSEPTFP 344

DB 299 TEILGILHSCNPLIYAFIGQKFRHGLKILAIHGLISKDSEPKDPSFVSGSSGHTST 358

QY 345 T 345

DB 359 T 359

RESULT 8

158186

probable G protein-coupled receptor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C/Accession: I58186

R/Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A/Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and b

A/Reference number: I58186; PMID:9433113; PMID:8047298

A/Accession: I58186

A/Status: preliminary; translated from GB/EMBL/DDBT

A/Molecule type: mRNA

A/Residues: 1-354 <RES>

A/Cross-references: EMBL:U04808; NID:G2558635; PIDN:AA87093.1; PID:G439861

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor

Query Match 28.8%; Score 524; DB 2; Length 354;

Best Local Similarity 36.9%; Pred. No. 1.8e-37;

Matches 113; Conservative 51; Mismatches 128; Indels 14; Gaps 4;

22 YDYSQYELICIKEDVEFAKVPFLVPLTVIVFVIGLAGNSVVAIYVYKQRTDVIIL 81

DB 13 FEYDDSAEACVLDIYAFGLIFLISFYSLVFTGLVGNLIVLATNRSKSKITDIYLL 72

QY 82 NLVADLLFLPFPMAVNAVHGWLTGKIMCKTSLTYLTFPSGMQFLACISIDRYAV 141

DB 73 NLASDILFVATLPFWHTYILSHGGLHNAKCTLPFFGFGGIFITVVISIDRYLA 132

QY 142 TKVPS-----OSGVGRKPCWIIICVMAAAILSPOLVFTVNDNACIPIPRYIGT 194

DB 133 VLAANSNNNTVQGV----TSLGVMAALITVASPQFMTFRKON-ELGIDYSEVLE 186

QY 195 SKRALIQMLEICGFVFPILMGVCFITRTLMKPNIKISPLKVLTVIVFIVTOL 254

DB 187 IWPVLRSEVNIIIGFVLPILIMSCYFRIVRTLFCKNRKKAIRILILVVVFPFLWT 246

QY 255 PYNIVFCRAIDIIISLITSCNMSKMDIAIQTESIALFHSCLNPLIVFENGASFKYV 314

DB 247 PYNIVFLETLK-FYNNFPGCGMKRDLRMALSTETVAFPSHCLNPLIYAFACEKFRRL 305

QY 315 MKYAKK 320

DB 306 RHLNKK 311

RESULT 9

JC4304

orphan G protein-coupled receptor - human

N/Alternate names: V28 protein

C/Species: Homo sapiens (man)

C/Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000

C/Accession: JC4304

R/Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.

Gene 163, 295-299, 1995

A/Title: The orphan G-protein-coupled receptor encoding gene V28 is closely related to g

A/Reference number: JC4304; PMID:96011651; PMID:7590284

A/Accession: JC4304

A/Molecule type: mRNA

A/Residues: 1-355 <RAP>

A/Cross-references: GB:U20350; NID:G665580; PIDN:AAA91783.1; PID:G665581

A:Experimental source: peripheral blood mononuclear cell
 C:Comment: This protein is a cell-surface receptor which recognizes extracellular signal
 C:Comment: This protein is a key regulator of many immune and homeostatic responses, and
 C:Genetics:
 A:Gene: v28
 A:Map position: 3pter-p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
 F:35-57/Domain: transmembrane #status predicted <TM1>
 F:66-88/Domain: transmembrane #status predicted <TM2>
 F:104-125/Domain: transmembrane #status predicted <TM3>
 F:146-165/Domain: transmembrane #status predicted <TM4>
 F:197-217/Domain: transmembrane #status predicted <TM5>
 F:230-254/Domain: transmembrane #status predicted <TM6>
 F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 28.7%; Score 522.5; DB 2; Length 355;
 Best Local Similarity 36.4%; Pred. No. 2.4e-37;
 Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;

QY 22 YDSQYELLCIKENVEFAKFLPVLTIVFVIGLAGNSMVAIYAYKKQRTQTVYLL 81
 DB 12 FEYDIAEACYIGIVGFVFIFSVFAIGVGNLIVFALTNKKPKSVTDIYLL 71
 QY 82 NLAVADLLFTLPFMAVNAHGVLGKIMCKITSALTYLNFVSGMOFLACISIDRYVAV 141
 DB 72 NLALSDLLFVALTPFWTHYLINKEGLNACKETTAFPIFGFSGIFFTIVISIDRYLAI 131
 QY 142 TKYPS-----QSGVKPCWIIICFCVMAAILLSIPQLVFYTVNDNARCIPIPRYLGT 194
 DB 132 VLAANSNNNTVHG-----TSLGWMAAILVAAPQFPTQKKN-ECLADYPEVLQ 185
 QY 195 SMKALIMELICIGFVVPFLIMGVCFITARTLMKNMNTISRLKVLTVVIVETQL 254
 DB 186 IMPVLAVRVEINFLGFLPLIMSCYFRIQTFCSCNKKAKAILILVIVFLEFMT 245
 QY 255 PYNIVFCRAIDIIYSLITSCNKRMDIAIQVTESIALFHSCLNPILYVFMGSPKNY 314
 DB 246 PYNMIFLETLK-LYDFPFCDMRKDIRALSVETEVAFSHCCLNPLIYVAFAEKERRYL 304
 QY 315 MKVAKKYG 322
 DB 305 YHL---YG 309

RESULT 10
 JC4587

C:Species: Mus musculus (house mouse)
 C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C:Accession: JC4587
 R:Hoogewest, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A:Reference number: JC4587; PMID:96136324; PMID:8573157
 A:Accession: JC4587
 A:Molecule type: mRNA
 A:Residues: 1-360 <HO>
 A:Cross-references: EMBL:X90862; NID:G1167851; PIDN:CAA62372.1; PID:G1167852

A:Experimental source: thymus
 C:Genetics:
 A:Gene: cc ckr-4
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F:2,183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 28.7%; Score 522.5; DB 2; Length 360;
 Best Local Similarity 33.7%; Pred. No. 2.5e-37;
 Matches 110; Conservative 69; Mismatches 128; Indels 19; Gaps 6;

QY 3 LEONSTDYVEENENGTVDYSQYELLCIKEDVEFAKFLPVLTIVFVIGLAGNSMV 62
 DB 1 KNAETDTDTQDEHYVNSGYFESMPKCTKEDGIAFAFEVFLPYSLVFLGLFGNSV 60
 QY 63 VAIVAYKKQRTQTVYLLNLAVALDLLFTLPFMAVNAHGVLGKIMCKITSALTYLN 122
 DB 61 VLVLFKRYLKMVTIVYLLNLAISDLFVLSLPFGVYAAQWFGDLCIKVSMWYLVG 120
 QY 123 FVSGMOFLACISIDRYVAVTKV-----PSOSGVKPCWIIICFCVMAAILLSIPQLV 175
 DB 121 FVSGIFLIMSIDRYLAIYHAFVSKRTILTYGV-----ITSLITWVAVAFASPLGLF 175
 QY 176 ---YVNDNARCIPIPRYLGTSMKALIQMEL-CIGFVVPFLIMGVCFITARTLMKP 231
 DB 176 STCYEHNHYCKQYS--VNSTWKVLSLEINVLGLIPLIGIMLFWYSMIIRTLQCK 233
 QY 232 NIKIRPFLKVLTVVIVFVITQLPYNIKFCRAIDIIYSLITSCNKRMDIAIQVTESI 291
 DB 234 NEKRAARMIFGVVVLFGMTPIYNVLFETL-VELLEVLDCTLERKYLDAIQATETL 292
 QY 292 ALFHSCLNPILYVFMGSPKNYMKV 317
 DB 293 GRFHCLNPIYVIFLGEKRRKYITQL 318

RESULT 11
 B57733

G protein-coupled receptor GPR2 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
 C:Accession: B57733
 R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, L.
 Genomics 23, 609-618, 1994
 A:Title: Cloning of human genes encoding novel G protein-coupled receptors.
 A:Reference number: B57733; PMID:95154831; PMID:7851889
 A:Accession: B57733
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-354 <MAR>
 A:Cross-references: GB:U13667

C:Genetics:
 A:Gene: GDB:GPR2
 A:Cross-references: GDB:371708; OMIM:600240
 A:Map position: 17q21.1-17q21.3
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 28.5%; Score 518.5; DB 2; Length 354;
 Best Local Similarity 33.9%; Pred. No. 5.4e-37;
 Matches 121; Conservative 65; Mismatches 142; Indels 29; Gaps 7;

QY 12 YVEENMGTDYSQYELLCIKEDVEFAKFLPVLTIVFVIGLAGNSMVAIY-AYK 70
 DB 5 HYSGD-EHAYSAPPELCEKADYQAFSPQSVSLVAALGAGVLAHTLAAR 63
 QY 71 KQRTQTVYLLNLAVALDLLFTLPFMAVNAHGVLGKIMCKITSALTYLNFVSGMOFL 130
 DB 64 AARSPTSNHLQIALADLLALTLPFAAGALQMSIGSATCRTISGLYASFAHGFLL 123
 QY 131 ACISIDRYVAVTKV-----PSOSGVKPCWIIICFCVMAAILLSIPQLVFYTVND--NAR 183
 DB 124 ACISADRYVAVTKVLPAGRPSTGR-AHLVSVYVWLSLALPALFSGDGRBQRR 182
 QY 184 CIPFPRYLGTSMKALIQMELICIGFVVPFLIMGVCFITARTLMKNPKISRLKVL 243
 DB 183 CRLIFPGLQYVAGAAVQVALGFLPLGVWVACVALLGRTTLARGPERRALRVV 242
 QY 244 TVVIVFVITQLPYNIKFCRAIDIIYSLITSCNKRMDIAIQVTESIALFHSCLNPI 303
 DB 243 ALVAFVVLQPLVSLALLDTADLARERSCPASKKDVALLVTSGLALARCGLNPLV 302
 QY 304 VFMGSPKNYMKVAK-----KYGSMRORQSVVEFPDSEGTPTSTFSI 350

Db 303 AAFGLFRODRLRLRGSSPSGQPRRCGPRRLS-----SCSAPETHTSL 350

RESULT 12

A53752

Interleukin-8 receptor (clone 5B1a) - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 05-Nov-1999

C/Accession: A53752

R/Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J. Biol. Chem. 269, 12391-12394, 1994

A/Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.

A/Reference number: A53752; MUID:94220294; PMID:8175642

A/Accession: A53752

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-358 <PRA>

A/Cross-references: GB:L24445; NID:9437661; PIDN:AAA1378.1; PID:9437662

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.1%; Score 511; DB 2; Length 358;

Best Local Similarity 32.3%; Pred. No. 2,4e-36;

Matches 116; Conservative 72; Mismatches 139; Indels 32; Gaps 8;

Qy 10 DYYEENEMNGTYDYGQYELI-----CIKEDVREFAKYFLPVFLTIVFVIGLA 57

Db 8 NYEYE--DFEG--DFENYSYSTDLPEPTLDSAPCRSESELTNSYVLITYI-LVLELLSL 62

Qy 58 GNSMVAIAIAYYKKQRTKTDVYLNLAVADLLFTLPFWAVNAVHGVGLKINKITSA 117

Db 63 GNSLWMLVILYSRSTCSVDVYLLNLAIADLLFATLPTMAASKVHGWTFGTPLCKVSL 122

Qy 118 LVTNLFVSGQGFACISIDRYAV-----TKVPSQSGVGKPCWICFCVMAAILLSIPQ 172

Db 123 VKENVYSSGLLACTSVDRYLAIVHATRTMIOKRLV---FICLSMGVSLLSLPI 178

Qy 173 LVEYTVNDNARCPIFFRYLGTG--MKALIQMLEICIGFVVVFLIMGVCFITARTMK 229

Db 179 LTRRNAIFPNSPVCEDMGNSTAKRWMLRLPQTGFILPLVLMLECYVFTLRTLFQ 238

Qy 230 MPRIKTSRLKXLLTVYVIVVQLKPNYVVKPCRAIDIIYSLTSCNMSKMDIAIQVTE 289

Db 239 AHWGQGRARAVFAVALLFLCLWLPYNLVLTDTIMRCHVIOETERNDDRLADATE 298

Qy 290 SIALLFHSCLNPILYVPMGASFKNYVMKVKYGMWRCQ--ROSVEEPFDESGEPTPT 345

Db 299 ILGLFHSCLNPIIYAFVIGQKFRYGLKLILAHGLISKEFLAKESRPSFVASSGNTSTT 357

RESULT 13

JQ1231

Interleukin-8 receptor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #ext_change 05-Nov-1999

C/Accession: JQ1231; A46483

R/Beckmann, M.P.; Munger, W.E.; Kozlowsky, C.; Vandenbos, T.; Price, V.; Lyman, S.; Gerard Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A/Title: Molecular characterization of the interleukin-8 receptor.

A/Reference number: JQ1231; MUID:91378994; PMID:1898400

A/Accession: JQ1231

A/Molecule type: DNA

A/Residues: 1-355 <BEC>

A/Cross-references: GB:M74240; NID:9165438; PIDN:AAA1375.1; PID:9165439

R/Dee, U.; Kuan, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A/Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.

A/Reference number: A46483; MUID:92148149; PMID:1737938

A/Accession: A46483

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-355 <BEC>

A/Cross-references: GB:M82873; NID:9165440; PIDN:AAA1376.1; PID:9165441

A/Experimental source: neutrophils

A/Note: Sequence extracted from NCBI backbone (NCBIN:81526, NCBIPI:81530)

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.6%; Score 501.5; DB 2; Length 355;

Best Local Similarity 33.1%; Pred. No. 1.5e-35;

Matches 107; Conservative 70; Mismatches 127; Indels 19; Gaps 6;

Qy 12 YEEENEMNGT-----YDYGQYELICIKEDVREFAKYFLPVFLTIVFVIGLAGNSMVAI 65

Db 14 WFEDEFANAGMPFVEKDY--PCLVYQTINKYVY--VIVAVFLSLTLCNSLWLV 68

Qy 66 YAYYKQRTKTDVYIINLAVADLLFTLPFWAVNAVHGVGLKINKITSAIYTLNFS 125

Db 69 ILSRNSRSTVDVYLLNLAVADLLFALTMTMAVSKRGKMFPTPLCKVSLKENVFIS 128

Qy 126 GMQPLACISIDRYAV-----TKVPSQSGVGKPCWICFCVMAAILLSIPQVLYVNDNA 182

Db 129 GILLLACTSVDRYLAIVHATRTLTQK--RLVVFICIGVIALSLTSLPEFLRQVSPN 186

Qy 183 RCLIFPRYIG---TSKALIQMLEICIGFVVVFLIMGVCFITARTMKMPRIKISRL 239

Db 187 NSSPVCEYEDGHNTAKRWMLRLPHTFGFILPLVLMLECYGFTLRTLFQAHWGQGRAM 246

Qy 240 KVLTVVIVFIVTQLPYNIVKPCRAIDIIYSLTSCNMSKMDIAIQVTEISALFHSCLN 299

Db 247 RVIAVVLILCLPFLNVLADTLMTHTVIGETQRRNDIRALDATEILGLFHSCLN 306

Qy 300 PLYVPMGASFKNYVMKVKYGMWRCQ--ROSVEEPFDESGEPTPT 345

Db 307 PIIYAFIGONFRNGFLMLAARG 329

RESULT 14

A45747

Neuropeptide Y/receptor Y3 - human

N/Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor YESTR; re

C/Species: Homo sapiens (man)

C/Date: 03-May-1994 #sequence_revision 03-May-1994 #ext_change 05-Nov-1999

C/Accession: A45747; A53103; 153006; 159444; 169203; S32761

R/Federerpiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schepet, K.; Clark-Lewis Genomica 16, 707-712, 1993

A/Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu

A/Reference number: A45747; MUID:93315164; PMID:8325644

A/Accession: A45747

A/Molecule type: mRNA

A/Residues: 1-352 <FRD>

A/Cross-references: GB:M92923; NID:9292516; PIDN:AAA16617.1; PID:9292517

R/Loetscher, M.; Geisler, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Noser, B. J. Biol. Chem. 269, 232-237, 1994

A/Title: Cloning of a human seven-transmembrane domain receptor, YESTR, that is highly e

A/Reference number: A53103; MUID:94103215; PMID:8276799

A/Accession: A53103

A/Molecule type: mRNA

A/Residues: 1-352 <LOB>

A/Cross-references: EMBL:X71635; NID:9297099; PIDN:CAA50641.1; PID:9297100

R/Herzog, H.; Hort, Y.J.; Shine, J.; Seible, L.A. DNA Cell Biol. 12, 465-471, 1993

A/Title: Molecular cloning, characterization, and localization of the human homolog to t

A/Reference number: 153006; MUID:93319629; PMID:8329116

A/Accession: 153006

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-352 <HER>

A/Cross-references: GB:106797; NID:9414929; PIDN:AAA03209.1; PID:9414928

R/Jaatin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Lar Regu. Pept. 47, 247-258, 1993

A/Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolo

A/Reference number: 159444; MUID:9405833; PMID:8274909

A/Accession: 159444

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:19 / Search time 18 seconds

(Without alignments)
1012.475 Million cell updates/sec

Title: US-09-721-341-2

Sequence: 1819
1 MAFEQNSTDYIYENENANG.....VEEPFDSGPEPTSTFSI 350

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1819	100.0	350	1 CKRB_HUMAN	Q9npb9 homo sapien
2	1620	89.1	350	1 CKRB_BOVIN	P35350 bos taurus
3	659	36.2	378	1 CKR7_HUMAN	P32248 homo sapien
4	650	35.7	378	1 CKR7_MOUSE	P47774 mus musculu
5	639	35.1	369	1 CKR9_MOUSE	Q9wut7 mus musculu
6	637	35.0	357	1 CKR9_HUMAN	P51686 homo sapien
7	605	33.3	367	1 CKR6_MOUSE	O54689 mus musculu
8	583	32.1	374	1 CKR6_HUMAN	P51684 mus musculu
9	581	31.9	342	1 CKR6_CERAE	O18983 cercopithec
10	571	31.4	343	1 CKR6_MACMU	Q9x452 macaca mula
11	569	31.3	343	1 CKR6_MACNE	O19024 macaca neme
12	566	31.1	343	1 CKR6_MACFA	Q9bd46 macaca fasc
13	560	30.8	342	1 CKR6_HUMAN	O00574 homo sapien
14	559	30.7	342	1 CKR6_PANTR	Q9tvi6 pan troglod
15	537.5	29.5	360	1 CKR4_HUMAN	P51799 homo sapien
16	534.5	29.4	360	1 ILB8_HUMAN	P25025 homo sapien
17	529.5	29.1	363	1 ILB8_PANTR	Q28807 pan troglod
18	527	29.0	384	1 CKD6_HUMAN	O00590 homo sapien
19	525	28.9	362	1 CKR4_HUMAN	P46092 homo sapien
20	524	28.8	354	1 CKR4_HUMAN	P46092 homo sapien
21	522.5	28.7	353	1 ILB8_GORGO	Q28411 fatuus novy
22	522.5	28.7	353	1 ILB8_GORGO	Q28412 gorilla gor
23	522.5	28.7	353	1 CKR4_HUMAN	P49338 homo sapien
24	521.5	28.7	353	1 CKR4_MOUSE	P51680 mus musculu
25	520.5	28.6	352	1 ILB8_MACMU	Q28519 macaca mula
26	512	28.1	356	1 ILB8_CANFA	Q9j121 mus musculu
27	511	28.1	354	1 ILB8_MOUSE	O92069 mus musculu
28	504	27.7	358	1 ILB8_PABIT	P35444 macaca mula
29	504	27.7	358	1 CKR4_MACMU	O18793 macaca mula
30	501.5	27.6	355	1 ILB8_PABIT	P21109 cryotolagus
31	501.5	27.6	358	1 CKR4_PABIT	Q92913 cavia porce
32	500.5	27.5	352	1 CKR4_HUMAN	P30091 homo sapien
33	499.5	27.5	353	1 CKR4_BOVIN	P25930 bos taurus

34	499.5	27.5	360	1 ILB8_BOVIN	Q28003 bos taurus
35	498.5	27.4	352	1 CCR4_PAPAN	P56491 papio ambi
36	498.5	27.4	352	1 CKR5_CERPO	O62743 cercopithec
37	498.5	27.4	353	1 CKR4_FELCA	P56498 felis silve
38	497.5	27.4	350	1 ILB8_GORGO	P55919 gorilla gor
39	495.5	27.2	352	1 CKR5_CERAE	O62747 cercopithec
40	494.5	27.2	352	1 CCR4_GORGO	O62747 cercopithec
41	493.5	27.1	352	1 CCR4_MACFA	Q28474 macaca fasc
42	493.5	27.1	352	1 CCR4_MACMU	P79394 macaca mula
43	492.5	27.1	359	1 CKR3_PABIT	O54814 fatuus novy
44	492.5	27.1	359	1 ILB8_PABIT	P35407 fatuus novy
45	491.5	27.0	352	1 CKR5_PAPHA	P56441 papio hamad

ALIGNMENTS

RESULT 1
ID CKRB_HUMAN STANDARD: PRT: 350 AA.
AC Q9NPB9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 11 (C-C CKR-11) (CC-CKR-11) (CCR-11)
DE (Chemokine receptor-like 1) (CRL1) (CCX CKR).
DE CCR1L OR CCR1L OR CCR1L OR CCR1L OR CCR1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20200450; PubMed=10734104;
RA Schweickart V.L., Epp A., Raport C.J., Gray P.W.;
RT "CCR11 is a functional receptor for the monocyte chemoattractant
protein family of chemokines.";
RL J. Biol. Chem. 275:9550-9556(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171478; PubMed=10706668;
RA Goshing J., Dairagh D.J., Wang Y., Hanley M., Talbot D., Miao Z.,
Schall T.J.;
RT "Identification of a novel chemokine receptor that binds dendritic
cell- and T cell-activating chemokines including ELC, SLC, and TECK.";
RL J. Immunol. 164:2851-2856(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231748; PubMed=10767544;
RA Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;
RT "Cloning of CCR11, an orphan seven transmembrane receptor related to
chemokine receptors, expressed abundantly in heart.";
RL Gene 246:229-238(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX Kopeck S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Receptor for SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4,
SCYA19/MIP3B/ETC, SCYA21/SLC and SCYA23/TECK.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: Predominantly expressed in heart. Lower
expression in lung, pancreas, spleen, small intestine and fetal
tissues.
CC - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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Db 1 MAVENSTIYVYENEMNDTHDSQYEVICIKKEVKKFVLPFAFTIAGLGS 60
Qy 61 MVAIVYVYKORRKPEDVYILINLAVADLLFLTPFAVNAVGVTKMCKITSAIT 120
Db 61 TTAIVYVYKRRKKTIVYILINLAVADLLFLTPFAVNAVGVTKMCKITSAIT 120
Qy 121 LNFVSGNQFIACISIDRYAVATKVPSSQGVGKPCWMIICPCWMAAILLSIPQLVFTVND 180
Db 121 VNFVSGNQFIACISIDRYAVATKVPSSQGVGKPCWMIICPCWMAAILLSIPQLVFTVNH 180
Qy 181 NARCIPIEPYVIGTSMKALLQMLEICGFVYVPHLMVCFTIARTMKMPNKISRPX 240
Db 181 KARCVPPIPHLGSMFASIQIIEICGFTIPLINAVCFITAKTLIKMPNKISQPK 240
Qy 241 VLLTVIVFTVTPQPNYIVKFCRAIDITVSLTSCMSKMDIAIQTVESIALFHSCLNP 300
Db 241 VLFVTVIVFTVTPQPNYIVKFCRAIDITVSLTSCMSKMDIAIQTVESIALFHSCLNP 300
Qy 301 ILVVFVGFASFRNYMKYAKKYGSMRORQVSEFPDSEPTPTSTFST 350
Db 301 VLVVFVGFASFRNYMKYAKKYGSMRORQVSEFPDSEPTPTSTFST 350

```

RESULT 3

```

ID CKR7_HUMAN STANDARD; PRT; 378 AA.
AC P32248;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7)
DE (MIP-3 beta-receptor) (EBV-induced G protein-coupled receptor 1)
DE (EB1) (BHR2)
GN CCR7 OR CMKR7 OR EB1 OR EVI1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
RA Kieff E.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.M.;
RT "Cloning of human and mouse EB1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Alteshul S.F., Zeeberg B., Buetow K.H., Schenker C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Matsuna K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Caranci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.U., Malek J.A., Gumatatue P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodighiero S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodighiero S.A.C., Grimwood J., Schmitt J., Myers R.M.,
RA Butterfield K.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
RA Schermer A., Schein U.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC - FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator
CC of EBV effects on B lymphocytes or of normal lymphocyte functions.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: Expressed in various lymphoid tissues and
CC activated B and T lymphocytes, strongly upregulated in B cells
CC infected with Epstein-Barr virus and T cells infected with
CC herpesvirus 6 or 7.
CC - INDUCTION: By EBV.
CC - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC -----
CC EMBL: L08176; AAS8615.1; -
CC EMBL: L31584; AAT74230.1; JOINED.
CC EMBL: L31583; AAT74230.1; JOINED.
CC EMBL: L31581; AAT74231.1; -
CC EMBL: BC093543; AAB5343.1; -
CC PIR: A45680; A45680.
CC PIR: B55735; B55735.
CC HSPB: P34996; 1DDP.
CC GeneW: HGNC:1608; CCR7.
CC MIM: 600242; -
CC GO: GO:0005887; C:Integral to plasma membrane; TAS.
CC GO: GO:0004950; F:chemokine receptor activity; TAS.
CC GO: GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO: GO:0006960; P:antimicrobial humoral response (sensu Inver. .); TAS.
CC GO: GO:0006935; P:chemotaxis; TAS.
CC GO: GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
CC GO: GO:0006954; P:inflammatory response; TAS.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm1.1.
CC PRINTS: PRO0237; GPCR_Rhodopsn.
CC PROSITE: PS00237; G-PROTEIN RECP F1_1.
CC PROSITE: PS0262; G-PROTEIN RECP F1_2; 1.
CC - G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24
CC CHAIN 25 378
CC DOMAIN 25 59
CC TRANSSEM 60 86
CC DOMAIN 87 95
CC TRANSSEM 96 116
CC DOMAIN 117 130
CC TRANSSEM 131 152
CC DOMAIN 153 170
CC TRANSSEM 171 191
CC DOMAIN 192 219
CC TRANSSEM 220 247
CC DOMAIN 248 263
CC TRANSSEM 264 289
CC DOMAIN 290 313
CC TRANSSEM 314 331
CC DOMAIN 332 378
CC CARBOHYD 336 36
CC DISULFID 129 210
CC CONFLICT 182 183
CC CONFLICT 337 337
CC SEQUENCE 378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;

```

Query Match 36.2%; Score 659; DB 1; Length 378;

Best Local Similarity 38.7%; Pred. No. 6,6e-34;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MLEGNOSDYEEENEMNGTYDSQYELICIKEDVEFAKFLPVFLTIVFGLAGNS 60
Db 21 VLCCQDEVDDIGNT---TVDYTLFBSLCKSKVNFPMFLPIMWSIICFGLGNG 77
QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVNLCKINCKITSLYT 120
Db 78 LVLLTYIYFKRLKMTDTLNLAVADLLFTLPFAVNAVHGVNLCKINCKITSLYT 137
QY 121 LNFVSGMGLACISIDRYAVATKVP---OSGVKPCMTIICFYMAALISIPOLVY 176
Db 138 MSFSGMMLLICISIDRYAVATKVP---OSGVKPCMTIICFYMAALISIPOLVY 197
QY 177 TVNDNA---RCIPFPRYIGTSKMLIQMLEICIGFVPEPLNGVCYFTARTLMKP 231
Db 198 DQSSSEQAMCSLITEH---VEAFITQVQWYIGFVPEPLNGVCYFTARTLMKP 254
QY 232 NIKISRPFLVLTIVVIFVITQLPYIVKFCRAIDIIYSLISGMSKRMIDAIQVTE 291
Db 255 NFERNAIVITAVVAVFVIFQLPNGVLAQTAVANTITSTCELSKQNLAIADVTSL 314
QY 292 ALFHSCLNPILYFMGASFKNYMKVAKYK---SW-----PRQSVSEFPD 337
Db 315 ACVRCGVNPFVAFIVKFRNDLFLKFDLGLSGLRQMSCHIRRSMSVE----- 369
QY 338 SEGPTPTSTFS 349
Db 370 ---AETTTFS 377

RESULT 4
CKR7_MOUSE STANDARD; PRT; 378 AA.

AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7)
DE (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
DE (EBI1)
GN CCR7 OR CMKBR7 OR EBI1 OR EBIH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=9514835; PubMed=7851893;
RA Schwickert V.L., Rubert C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT Cloning of human and mouse EBI1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2;
RT Genomics 23:643-650 (1994).
RL
CC -|- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator
CC of EBV effects on B lymphocytes or of normal lymphocyte functions.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: L31580; AAA74232.1; -
DR PIR: A55735; A55735;
DR MGD: MGI:103011; Ccr7
DR GO: 0016493; F:C-C chemokine receptor activity; IMP.

DR GO: 0006935; P:chemotaxis; IMP.
DR GO: 0006955; P:immune response; IMP.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 378
FT DOMAIN 25 59
FT TRANSSEM 60 86
FT DOMAIN 87 95
FT TRANSSEM 96 115
FT DOMAIN 117 130
FT TRANSSEM 131 152
FT DOMAIN 153 170
FT TRANSSEM 171 191
FT DOMAIN 192 219
FT TRANSSEM 220 247
FT DOMAIN 248 263
FT TRANSSEM 264 289
FT DOMAIN 290 313
FT TRANSSEM 314 337
FT DOMAIN 332 378
FT CARBOHYD 36 36
FT DISULFID 129 210
SQ SEQUENCE 378 AA; 42941 MW; ACB1A422CF54AAB54 CRC64;

Query Match 35.7%; Score 650; DB 1; Length 378;
Best Local Similarity 38.3%; Pred. No. 2,4e-33;
Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

QY 5 QNOSTDYEEENEMNGTYDSQYELICIKEDVEFAKFLPVFLTIVFGLAGNSMVA 64
Db 25 QDEVTDYIGENT---TVDYTLFBSLCKSKVNFPMFLPIMWSIICFGLGNGVIL 81
QY 65 IVAYYKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVNLCKINCKITSLYTIN 124
Db 82 TYIYFKRLKMTDTLNLAVADLLFTLPFAVNAVHGVNLCKINCKITSLYTIN 141
QY 125 SGMOFLACISIDRYAVATKVP---VSKPCMTIICFYMAALISIPOLVY 177
Db 142 SGMLLICISIDRYAVATKVP---VSKPCMTIICFYMAALISIPOLVY 198
QY 178 VNDNA---RCIPFPRYIGTSKMLIQMLEICIGFVPEPLNGVCYFTARTLMKP 230
Db 199 LQKSGEDTLRC---SLVSAQVEALITIQVQWYIGFVPEPLNGVCYFTARTLMKP 253
QY 231 NIKISRPFLVLTIVVIFVITQLPYIVKFCRAIDIIYSLISGMSKRMIDAIQVTE 290
Db 254 NFERNAIVITAVVAVFVIFQLPNGVLAQTAVANTITSTCELSKQNLAIADVTSL 313
QY 291 IALFHSCLNPILYFMGASFKNYMKVAKYKSWROR-----OSVEEFPDSEPT 343
Db 314 LASVRCGVNPFVAFIVKFRNDLFLKFDLGLSGLRQMSCHIRRSMSVE---AE 371
QY 344 PTSTFS 349
Db 372 TTTTFS 377

RESULT 5
CKR9_MOUSE STANDARD; PRT; 369 AA.

AC Q9WUT7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 9 (C-C CKR-9) (CCR-9)
DE (Chemokine C-C receptor 10).
GN CCR9 OR CMKBR10.
OS Mus musculus (Mouse).


```

CC EMBL: U45982; AAA93319.1; -.
DR EMBL: AY242127; AAO92294.1; -.
DR Genem: HGNC:1510; CCR6.
DR MIM: 604738; -.
DR GO: GO:0005877; C: integral to plasma membrane; TAS.
DR GO: GO:0004950; F: chemokine receptor activity; TAS.
DR GO: GO:0006968; P: cellular defense response; TAS.
DR GO: GO:0006935; P: chemotaxis; TAS.
DR GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
DR GO: GO:0007186; P: G-protein coupled receptor protein signaling. .; TAS.
DR InterPro: IPR004069; CC_9_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1531; CHEMOKINER9.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 37
FT TRANSMEM 38 64
FT DOMAIN 65 73
FT TRANSMEM 74 94
FT TRANSMEM 95 108
FT TRANSMEM 109 130
FT TRANSMEM 131 148
FT TRANSMEM 149 169
FT DOMAIN 170 198
FT TRANSMEM 199 226
FT TRANSMEM 227 242
FT TRANSMEM 243 268
FT TRANSMEM 269 292
FT TRANSMEM 293 310
FT TRANSMEM 311 357
FT CARBOHYD 20 20
FT DISULFID 107 186
SQ SEQUENCE 357 AA; 40713 MW; 96982E0B922FEB31 CRC64;

Query Match 35.0%; Score 637; DB 1; Length 357;
Best Local Similarity 36.5%; Pred. No. 1.4e-32;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DYYEE-NEMNGTYDSQYELL-CKEDVREFAKFLPFLTLIVVIGLNGSMVAIYAY 68
DB 4 DYSESSTSSMEDVYVNFPTDFCEKQNVROFASHFLPYLVIFVIGALNSLIVLVY 63
QY 69 YKQRTKTYVILNLAVALDILLFLTPPAVNAVHGWLGKIMCKITSLATLNFVSGM 128
DB 64 CTREKMTMDLFLNLIALDLFLVTLPEFAIAADQMKQTEFCKVNSMYKMFYCVL 123
QY 129 FLACISIDRYVAATKVPSSQSGVPCW-----IICFVMAAILSLIPQVETVYN 179
DB 124 LINCISIDRYIAIAQ-----AMRAHWREKRLYSKWCCTIVVLAALCIPILYSQIK 178
QY 180 DN--ARCFIPFYLYSTKALIQMLEICIGVAVPFLINGVCFYFTAKIMKPIKIS 236
DB 179 EESGIAICIMVYPSDESTKLKSAVLTLLKVLGFELPFWAACCYTIIHPTLQAKSSRH 238
QY 237 RPLKVLTLVIVVIVLQPLFYNIKFCRAIDITSLTSCMSKMDIAICVESIALFHS 296
DB 239 KALKVTLITLVIVLVSFPFNCILIVOTIDAYAMFISNCVSNINDICGVYOTIAFHS 298
QY 297 CLNPILVFGASFKYVNVKAKYK 322
DB 299 CLNPILVFVGEFRRLDVLVTKNLIG 324

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DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 6 (C-C CKR-6) (CC-CCR-6) (CCR-6) (KX411).
GN CCR6 OR CCKR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yanagihara S., Komura E., Yamaguchi Y.,
RA Valtonen R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
RA Albar J.P., Ardavin C., Marquez G.,
RT "Molecular cloning, functional characterization and mRNA expression
RT analysis of the murine chemokine receptor CCR6 and its specific ligand
RT MIP-3alpha".
RT FEBS Lett. 440:188-194 (1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-
CC alpha/LARC and subsequently transduces a signal by increasing the
CC intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
CC
CC EMBL: AB009369; BA23776.1; -.
DR EMBL: AJ222714; CA10956.1; -.
DR MGD: MGI:133797; Ccr6.
DR GO: GO:0005515; F: protein binding; IPI.
DR InterPro: IPR004067; CC_6_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1529; CHEMOKINER6.
DR PROSITE: PS00237; GPCR_Rhodopsn.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39
FT TRANSMEM 40 66
FT TRANSMEM 67 75
FT TRANSMEM 76 96
FT TRANSMEM 97 111
FT TRANSMEM 112 133
FT TRANSMEM 134 151
FT TRANSMEM 152 172
FT TRANSMEM 173 203
FT TRANSMEM 204 230
FT TRANSMEM 231 246
FT TRANSMEM 247 271
FT TRANSMEM 272 295
FT TRANSMEM 296 313
FT TRANSMEM 314 367
FT DISULFID 110 189
FT CARBOHYD 2 2
FT CARBOHYD 35 35
SQ SEQUENCE 367 AA; 42102 MW; 6A309AF83B117E CRC64;

Query Match 33.3%; Score 605; DB 1; Length 367;
Best Local Similarity 37.9%; Pred. No. 1.3e-30;
Matches 129; Conservative 60; Mismatches 125; Indels 26; Gaps 8;

QY 8 STDYYEENMNGTYDSQYELL-CKEDVREFAKFLPFLTLIVVIGLNGSM 61

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DB 3 STEBYFETDD----YDNTVEYSIPDPGSLERVNFVPIAVSLICVGLIGNIM 58
 QY 62 VVAIYAYKKORTKTDVYIINLAVADILLFTLPFMAV-NAVHGWLGKIMKITSALYT 120
 DB 59 VVMFAYKARSWMTDYLINMATDILLFTLPFMAVTAHTWVSDSLCMLMGTYA 118
 QY 121 LNFVSGQFIACISIDRYVAVTKVPSQSGVGPCKW----IICCVMAAILISIPOLVF 175
 DB 119 VNRFCGLLLACISMRYIAIVQATKTSFRFRSRRLTHSKYICAAVMFISITISSPFIIN 178
 QY 176 --YTVNDNARCIPIFPYLGTS---NKALICMLICIGFVPELIMGVCYFITARTLTK 229
 DB 179 KRYELQCRDVC---EPYRSVSEBITWKLGMGLHLPFGFPTLLFNVCYLPITITVQ 235
 QY 230 MPNKRIRPKVLLTVIVIVFVQLPYNYKFCRAIDITISLTCMSKRMIAQVTE 289
 DB 236 AONSKRRHRAIRVAVLAVLFLACIPHNWVLVTAVA-TSKVRSCSTKTEVLAATRVAAE 294
 QY 290 SIALFHSCLNPILYFVNGASFKNYVMKAKKYGSRORQ 329
 DB 295 VLAFLHCCNPVLVYAFIGQKFRNVEFKIMEDVCMRKNK 334

RESULT 8
 CKRE_HUMAN STANDARD; PRT; 374 AA.
 AC PS1684; P78553; Q92846;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 6 (C-C CKR-6) (CCR-6) (LARC
 DE receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CCR-L3)
 DE (DRY6).
 GN CCR6 OR CCKBR6 OR STRL22 OR GPR29 OR CKRL3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI TaxID:9606;
 RX MEDLINE=97313465; PubMed=9169459;
 RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
 RA Nomiyama H., Yoshie O.,
 RT "Identification of CCR6, the specific receptor for a novel
 RT lymphocyte-directed CC chemokine LARC.";
 RL J. Biol. Chem. 272:14893-14898 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RL Lautens L.L., Modi W., Bonner T.I.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=886020;
 RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCoy R., Perlmutter D.H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224503; PubMed=9070937;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180 (1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction

RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22935763; PubMed=14574404;
 RA Munnell A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Burford D.C., Burdill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
 RA Collier R.E., Collins J.E., Coleman L.K., Corby N.R., Coville G.J.,
 RA Culley K.M., Dhami P., Davies J., Dunn M., Barthrowl M.E.,
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
 RA Gilby L.M., Gillson C.J., Githero R.J., Grafham D.V., Grant M.,
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
 RA Holmes S.V., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 RA Humphrey S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 RA Maeslen G.L., Matthews L., McCann C.T., McLaren S.J., McMay K.,
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
 RA Porter K.M., Ramsey Y., Randy S.A., Rice C.M., Ross M.T., Searle S.M.,
 RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
 RA Squeares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L., Whitaker H., Wild A., Willey D.V., Wilmer T.E., Wood J.M., Wray P.W.,
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
 RT "The DNA sequence and analysis of human chromosome 6.";
 RL Nature 425:805-811 (2003).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantinai P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko T., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalloe D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16889-16903 (2002).
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-
 CC intracellular calcium ions level.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- TISSUE SPECIFICITY: Spleen, lymph nodes, appendix, and fetal
 CC liver. Expressed in lymphocytes, T cells and B cells but not in
 CC natural killer cells, monocytes or granulocytes.
 CC -I- INDUCTION: By interleukin-2.
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

FT TRANSMEM 144 164 4 (POTENTIAL).
 FT DOMAIN 165 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 188 215 5 (POTENTIAL).
 FT DOMAIN 216 231 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 232 259 6 (POTENTIAL).
 FT DOMAIN 260 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 293 7 (POTENTIAL).
 FT DOMAIN 294 342 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 102 180 BY SIMILARITY.
 FT CARBOHYD 16 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 342 AA; 39226 MM; 6CBE389C6E5919E CRC64;

Query Match 31.9%; Score 581; DB 1; Length 342;
 Best Local Similarity 34.2%; Pred. No. 3.7e-29;
 Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps 8;

QY 12 YEENENMGTYDYSQYELICKEDEYREFAKVPFLVETIVFVIGLAGNSVVAIYAYKK 71
 DB 6 HYEDNGFNSFNDSQEE---HDFLQFSKVFPCMYLVVCGVGNSTLVVISIFYKH 61
 QY 72 QRTKTDVYILNLAADLLFTLPFWANAVHGVGLKIMKITSALYTNFVSGMFLA 131
 DB 62 LOSLTIVFLVPLADLVFVCTLPFWAYAGIHMIFGVWCKTLGITYTNFYSMLLT 121
 QY 132 CISIDRYVAATKVPB--QSGVGKPCW--ITCFYMAAILLSIPQVFTV--NDNARCI 185
 DB 122 CTVDRFIVVYKATKAYNOQAKMTGWKVICLLIWSILVSLPQIITYGNVFNLDKIC- 180
 QY 186 PIFPRYLGTSKALIQMLEICIGVVPFLNGVCYFITTARTLMKMPNIKSRPLKVLTV 245
 DB 181 ---GYHDEISTVLTATQMTLGFPLAMIVCYSVIKTLHAGGFQKRSIKITFLV 236
 QY 246 VIVEVITQLPYNIYKFCRAIDIIYSLTSCNMSKMDIAIQVTSIALFHSCLNPILYVF 305
 DB 237 MAVFLITQTPNIVKYLIRSTHMEYAMTSFHYT-----IIVTAIAYLRACINPVLYAF 290
 QY 306 MGASFKNYKVKVAKKYG-----SMRQROSVVEFPDSEPTPTSTFSI 350
 DB 291 VSLKFRKFMKLVKDIGCLPYLGVSHOKSSEDSNKK--TFSASHNVATSMFQL 342

RESULT 10

CCRE6_MACNU STANDARD; PRT; 343 AA.
 AC 09X143;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled
 DE receptor bonzo) (G protein-coupled receptor STRL33).
 GN CXCR6 OR BONZO OR STRL33.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxId=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Haber D.A., Clements J.E.,
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -1- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a
 CC coreceptor by HIV and by strains of HIV-2 and m-tropic HIV-1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF124380; AAD31419.1; -
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS02622; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 33
 FT TRANSMEM 34 60
 FT TRANSMEM 61 69
 FT TRANSMEM 70 90
 FT TRANSMEM 91 104
 FT TRANSMEM 105 126
 FT TRANSMEM 127 144
 FT TRANSMEM 145 165
 FT TRANSMEM 166 188
 FT TRANSMEM 189 216
 FT TRANSMEM 217 232
 FT TRANSMEM 233 260
 FT TRANSMEM 261 276
 FT TRANSMEM 277 294
 FT TRANSMEM 295 343
 FT CARBOHYD 17 17
 FT DISULFID 103 181
 SQ SEQUENCE 343 AA; 39423 MM; 48B2544949EB83F CRC64;

Query Match 31.4%; Score 571; DB 1; Length 343;
 Best Local Similarity 33.4%; Pred. No. 1.5e-28;
 Matches 119; Conservative 73; Mismatches 132; Indels 32; Gaps 8;

QY 10 DYEEENMGTYDYSQYELICKEDEYREFAKVPFLVETIVFVIGLAGNSVVAIYAY 69
 DB 5 DYEDNGFNSFNDSQEE---HDFLQFSKVFPCMYLVVCGVGNSTLVVISIFYKH 60
 QY 70 KQRTKTDVYILNLAADLLFTLPFWANAVHGVGLKIMKITSALYTNFVSGMFL 129
 DB 61 HKLQSLTDFVNLPLADLVFVCTLPFWAYAGIHMIFGVWCKTLGITYTNFYSMLI 120
 QY 130 LACISIDRYVAATKVPB--QSGVGKPCW--ITCFYMAAILLSIPQVFTV--NDNAR 183
 DB 121 LTCITVDRIIVVYKATKAYNOQAKMTGWKVICLLIWSILVSLPQIITYGNVFNLDKIL 180
 QY 184 CIPFPRYLGTSKALIQMLEICIGVVPFLNGVCYFITTARTLMKMPNIKSRPLKVL 243
 DB 181 C---GYHDEISTVLTATQMTLGFPLAMIVCYSVIKTLHAGGFQKRSIKITFLV 235
 QY 244 TVIVVITQLPYNIYKFCRAIDIIYSLTSCNMSKMDIAIQVTSIALFHSCLNPILY 303
 DB 236 LVMAVFLITQTPNIVKYLIRSTHMEYAMTSFHYT-----IIVTAIAYLRACINPVLY 289
 QY 304 VFMGASFKNYKVKVAKKYG-----SMRQROSVVEFPDSEPTPTSTFSI 350
 DB 290 AFVSLKFRKFMKLVKDIGCLPYLGVSHOKSSEDSNKK--TFSASHNVATSMFQL 343

RESULT 11

CCRE6_MACNE STANDARD; PRT; 342 AA.
 AC 019024;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled
 DE receptor bonzo).
 GN CXCR6 OR BONZO.
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxId=9545;

Db 61 HKQSLTVLVLNPLADLVFCTLPFWYAGIHENIFQWCKLLGVYITINFTSMLI 120
 QY 130 LACISIDRYAVATKVPSS--QSGVGKPCW--IICFCVWMAAILSTIPOLVFYTV--NDNAR 183
 Db 121 LNCITADRIIVVAKTKATKANOQAKMTKRVCLILNIVSLVSLPQITIGVNFMDKLI 180
 QY 184 CIPIDFPRYIGTSMKALICQMLEICIGFVDFPILMGVCYFITAFTLMKPNIKISPLKVL 243
 Db 181 C-----GYHDEHSITVATATQMTLGFPLMLAMICYSVIITLLHAGQFGHRSKLIIF 235
 QY 244 TVIVIVITQLPYNIYKFCRAIDIIISLTSCNMSKMDIAIQVESTALPHSCINPILY 303
 Db 236 LMAVAVLLIQTFFNLVKLIRSTRMEYANTSPHYT-----ITVEALAYLRACINPVLV 289
 QY 304 VFMGASFKYVYKVAKKYG-----SWRROROSVEEPDSEGPTEPTSPESI 350
 Db 290 AFVSLTKFRKNFMVLVDICLPLGVSHQWKSSEDNSK--TTSASHNVEATSMFQL 343
 RESULT 13
 CCR6_HUMAN
 ID CCR6_HUMAN STANDARD; PRT; 342 AA.
 AC 000574; 000575;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
 DE receptor bonzo) (G protein-coupled receptor STRL33).
 GN CXCR6 OR BONZO OR STRL33 OR TYMSTR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97373958; PubMed=9230441;
 RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
 RA "Expression cloning of new receptors used by simian and human
 RA immunodeficiency viruses.";
 RA Nature 388:296-300(1997).
 RL [2]
 RN SEQUENCE FROM N.A., AND VARIANT ALA-25.
 RA MEDLINE=97311099; PubMed=9166430;
 RA Liao F., Alkhatib G., Paden K.W.C., Sharma G., Berger E.A.,
 RA Farber J.M.;
 RA "STRL33, A novel chemokine receptor-like protein, functions as a
 RA fusion cofactor for both macrophage-tropic and T cell line-tropic
 RA HIV-1.";
 RA J. Exp. Med. 185:2015-2023(1997).
 RL [3]
 RN SEQUENCE FROM N.A.
 RA TISSUE=Blood;
 RA MEDLINE=97431687; PubMed=9285716;
 RA Loetscher M., Amara A., Oberlin B., Braas N., Legler D.F.,
 RA Baggiolini M., Arenzana-Seisdedos F., Moser B.;
 RA "TYMSTR, a putative chemokine receptor selectively expressed in
 RA activated T cells, exhibits HIV-1 coreceptor function.";
 RA Curr. Biol. 7:652-660(1997).
 RL [4]
 RN SEQUENCE FROM N.A.
 RA Kopecký S.A., Atkinson R.S., Sharma S.V.;
 RA "cDNA clones of human proteins involved in signal transduction
 RA sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RN SEQUENCE FROM N.A.
 RA TISSUE=pancreas;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.W., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stedilton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Cantucci P., Prange C.J.,
 RA Rana S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.J., Melex J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smellus D.E.,
 RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RA human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a
 CC coreceptor by SIV and by strains of HIV-2 and m-tropic HIV-1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in lymphoid tissues and activated T
 CC cells.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL: AF007545; AAB64221.1; -.
 DR EMBL: U73529; AAB61456.1; -.
 DR EMBL: U73531; AAB61457.1; -.
 DR EMBL: Y13248; CAA73698.1; -.
 DR EMBL: AY322543; AAB84356.1; -.
 DR EMBL: BC033584; AAP83584.1; -.
 DR Genbank: HGNC:16647; CXCR6.
 DR MIM: 605163; -.
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0015026; F: coreceptor activity; TAS.
 DR GO: GO:0004930; F: G-protein coupled receptor activity; TAS.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signaling. . . ; TAS.
 DR GO: GO:0008166; P: viral replication; TAS.
 DR InterPro: IPR00276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm1.1.
 DR PRINTS: PR00237; GPCR_RHOPOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 FT DOMAIN 1 32
 FT TRANSSEM 33 59
 FT DOMAIN 60 68
 FT TRANSSEM 69 89
 FT DOMAIN 90 103
 FT TRANSSEM 104 125
 FT DOMAIN 126 143
 FT TRANSSEM 144 164
 FT DOMAIN 165 187
 FT TRANSSEM 188 215
 FT DOMAIN 216 231
 FT TRANSSEM 232 259
 FT DOMAIN 260 275
 FT TRANSSEM 276 293
 FT DOMAIN 294 342
 FT DISULFID 102 180
 FT CARBOHYD 16 16
 FT VARIANT 25 25
 SQ SEQUENCE 342 AA; 39280 MW; 9FBC02556D1082E CRC64;
 /FTID=VAR_003506.
 Query Match 30.8%; Score 560; DB 1; Length 342;
 Best Local Similarity 33.1%; Pred. No. 7, 1e-28;

Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

QY 12 YEEENMGATGYSQYELICIKEDVEEPAKFLPVFLTIVFVIGLAGSMVAIYAYKK 71
 DB 6 YHEDGFSFNDSSQEE---HODPLQSKVFLPCMYLVVFGVGLVGNLSLVVISIFHK 61

QY 72 ORKTDVYILNIAVADLLFLTPFAVANAAGVGLKIMCKITSALYTLNFSGMOFLA 131
 DB 62 LQSLTDVFLVNLPLADLVFVCTLPFAVAGIHEWFGVWCKSLIGIYITINFTSMILT 121

QY 132 CISIDRYAVATKVPB--QSGVGKPCW--IICFCVMAAILISIPOLVFTV--NDNARCI 185
 DB 122 CITVDFRIVVATKATAYNOQAKMTGKTSLLIWLISLVLSQIIGVFNIDKLC- 180

QY 186 PIFPRYLGTSKRALIQMLEICIGFVFPFLIMGVCYFITARLTMKNPKISRLKXLLTV 245
 DB 181 ---GYHDEAISTVLATQMTLGFPLPLTMIVCYSVILIKTLHAGGFQKRSKLIIFLV 236

QY 246 VIVFIVTQLPYNIYVRCALDIYSLTSCNMSKMDIAIQVTSIALFHSCLNPLIYVF 305
 DB 237 MAVFLITQMPFNLMKIRSTHWEYAMTSFHT-----IMVTERIAYIRACLNPLIYVF 290

QY 306 MGASFKNVYWKVAKKYG-----SWRQROSVVEEPPDSEGPTEPTSTFSI 350
 DB 291 VSLKFRKNFWKLVKDIGCLPYLGSHQWKSSEDNSK--TFASHNVEATSMFOL 342

FT TRANSEM 104 125 3 (POTENTIAL).
 FT DOMAIN 126 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 144 164 4 (POTENTIAL).
 FT DOMAIN 165 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 188 215 5 (POTENTIAL).
 FT DOMAIN 216 231 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 232 259 6 (POTENTIAL).
 FT DOMAIN 260 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 276 293 7 (POTENTIAL).
 FT DOMAIN 294 342 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 102 180 BY SIMILARITY.
 FT CARBOHYD 16 16 N-LINKED (GCMAC. ...) (POTENTIAL).
 SQ SEQUENCE 342 AA; 39273 MW; 5586003797806B2A CRC64;

Query Match 30.7%; Score 559; DB 1; Length 342;
 Best Local Similarity 33.1%; Pred. No. 8.2e-28;
 Matches 117; Conservative 74; Mismatches 131; Indels 32; Gaps 8;

QY 12 YEEENMGATGYSQYELICIKEDVEEPAKFLPVFLTIVFVIGLAGSMVAIYAYKK 71
 DB 6 YHEDGFSFNDSSQEE---HODPLQSKVFLPCMYLVVFGVGLVGNLSLVVISIFHK 61

QY 72 ORKTDVYILNIAVADLLFLTPFAVANAAGVGLKIMCKITSALYTLNFSGMOFLA 131
 DB 62 LQSLTDVFLVNLPLADLVFVCTLPFAVAGIHEWFGVWCKSLIGIYITINFTSMILT 121

QY 132 CISIDRYAVATKVPB--QSGVGKPCW--IICFCVMAAILISIPOLVFTV--NDNARCI 185
 DB 122 CITVDFRIVVATKATAYNOQAKMTGKTSLLIWLISLVLSQIIGVFNIDKLC- 180

QY 186 PIFPRYLGTSKRALIQMLEICIGFVFPFLIMGVCYFITARLTMKNPKISRLKXLLTV 245
 DB 181 ---GYHDEAISTVLATQMTLGFPLPLTMIVCYSVILIKTLHAGGFQKRSKLIIFLV 236

QY 246 VIVFIVTQLPYNIYVRCALDIYSLTSCNMSKMDIAIQVTSIALFHSCLNPLIYVF 305
 DB 237 MAVFLITQMPFNLMKIRSTHWEYAMTSFHT-----IMVTERIAYIRACLNPLIYVF 290

QY 306 MGASFKNVYWKVAKKYG-----SWRQROSVVEEPPDSEGPTEPTSTFSI 350
 DB 291 VSLKFRKNFWKLVKDIGCLPYLGSHQWKSSEDNSK--TFASHNVEATSMFOL 342

RESULT 14

CCR6 PANTR STANDARD; PRT; 342 AA.

AC Q9TV16;
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33).
 GN CXCR6 OR BONZO OR STRL33.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9433499; PubMed=10505680;
 RA Brussel A., Preter J.-L., Girard M., Butor C.;
 RT "Sequences and predicted structures of chimpanzee STRL33 (Bonzo) and gp135 (BOB).";
 RL AIDS Res. Hum. Retroviruses 15:1315-1319(1999).
 CC -1- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC EMBL; AF084229; AAD52041.1; -
 DR InterPro; IPR000276; GPCR_rhodopsin.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PR00237; GPCRHHOOPS.N.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE; PS02622; G_PROTEIN_RECPT_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32
 FT TRANSEM 33 59 1 (POTENTIAL).
 FT DOMAIN 60 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 103 EXTRACELLULAR (POTENTIAL).

RESULT 15

CCR4 HUMAN STANDARD; PRT; 360 AA.

AC P51679; Q9ULY6; Q9ULY7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 4 (C-C CCR-4) (CCR-4) (CCR4) (KS-5).
 GN CCR4 OR CCR4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95370289; PubMed=7642634;
 RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.D., Proudfoot A.E.I., Wells T.N.C.;
 RT "Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.";
 RL J. Biol. Chem. 270:19495-19500(1995).
 CC This entry is part of a family of proteins.
 RN [2]
 RP SEQUENCE FROM N.A. AND VARIANTS VAL-130 AND SER-178.
 RX MEDLINE=21040311; PubMed=11196669;
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H., Hirai K., Tokunaga K.;
 RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
 RL Genes Immun. 1:97-104(1999).

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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:19 / Search time 45 Seconds
(without alignments)
2454.030 Million cell updates/sec

Title: US-09-721-341-2
Perfect score: 1819
Sequence: 1 MALENGSTDYVHEENMNG.....VRRPFDSEGPTEPTSTPSI 350

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPREMBL_25:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1596	87.7	350	11 Q92413	Q92413 mus musculus
2	1594	87.6	350	11 Q8C0M1	Q8C0M1 mus musculus
3	1593	87.6	350	11 Q8Q2W9	Q8Q2W9 mus musculus
4	912	50.1	221	11 Q9ESX1	Q9ESX1 rattus norv
5	657	36.1	378	6 Q8HZR6	Q8HZR6 macaca mula
6	646	35.6	378	11 Q8CASS2	Q8CASS2 mus musculus
7	645.5	35.5	380	6 Q8G1S1	Q8G1S1 sus scrofa
8	643	35.3	369	4 Q9U0Q6	Q9U0Q6 homo sapien
9	643	35.3	369	11 Q8CH33	Q8CH33 rattus norv
10	611	33.6	367	11 Q9R1V0	Q9R1V0 mus musculus
11	586.5	32.2	368	13 Q42444	Q42444 oncorhynch
12	583	32.1	374	6 Q8HZR7	Q8HZR7 macaca mula
13	578	31.8	343	6 Q9N0Z0	Q9N0Z0 cercopithec
14	566.5	31.1	351	11 Q9B016	Q9B016 mus musculus
15	566	31.1	343	6 Q9BDS6	Q9BDS6 macaca fasc
16	561.5	30.9	351	11 Q9ERH5	Q9ERH5 mus musculus

17	560	30.8	342	4 Q9HCAS	Q9HCAS homo sapien
18	559	30.7	342	6 Q9TV16	Q9TV16 pan troglod
19	544	29.9	358	13 Q9PUA0	Q9PUA0 acipenser r
20	535.5	29.4	355	6 Q8HZN7	Q8HZN7 gorilla gor
21	534.5	29.4	355	4 Q8IUZ1	Q8IUZ1 homo sapien
22	534.5	29.4	355	6 Q8HZN8	Q8HZN8 pan troglod
23	534.5	29.4	355	6 Q8HZN6	Q8HZN6 pongo pygma
24	531.5	29.2	360	6 Q8MJM8	Q8MJM8 canis famil
25	529	29.1	361	11 Q8VHP3	Q8VHP3 cavia porce
26	527	29.0	364	4 Q8GUNS	Q8GUNS homo sapien
27	525.5	28.9	360	11 Q91ZH4	Q91ZH4 rattus norv
28	521.5	28.7	358	13 Q7XUJ7	Q7XUJ7 xenopus lae
29	520.5	28.6	358	13 Q9YGC3	Q9YGC3 xenopus lae
30	516.5	28.4	355	6 Q8HZN3	Q8HZN3 papio hamad
31	516	28.4	355	11 Q9JLY8	Q9JLY8 rattus norv
32	515	28.3	364	4 Q7Z711	Q7Z711 homo sapien
33	513	28.2	354	11 Q8CBU0	Q8CBU0 mus musculus
34	511	28.1	354	11 Q8BR50	Q8BR50 mus musculus
35	508	27.9	355	6 Q8HZN5	Q8HZN5 macaca mula
36	507.5	27.9	347	6 Q9MZN1	Q9MZN1 eulemur mac
37	507	27.9	357	13 Q42445	Q42445 oncorhynch
38	506.5	27.8	347	6 Q9MZN6	Q9MZN6 calliscep
39	506.5	27.8	347	6 Q9MZN7	Q9MZN7 calliscep
40	505.5	27.8	355	6 Q8HZN4	Q8HZN4 cercopithec
41	505.5	27.8	374	13 Q80ZHI	Q80ZHI petromyzon
42	503.5	27.7	347	6 Q9MZN0	Q9MZN0 alouatta se
43	503.5	27.7	352	6 Q9TV44	Q9TV44 cercopithec
44	502.5	27.6	347	6 Q9MZP1	Q9MZP1 mandillus
45	502.5	27.6	347	6 Q9MZN5	Q9MZN5 pithecia pi

ALIGNMENTS

RESULT 1

ID Q92413 PRELIMINARY; PRT; 350 AA.

AC Q92413 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mus musculus (Mouse).
CN CCR1L
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20519697; PubMed=11063828;
RA "Doit M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.,
RT "Astrocytes express functional chemokine receptors.";
RL J. Neuroimmunol. 111:109-121(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
EMBL: AF306532; AAK81712.1; -;
EMBL: AK042430; BAC31258.1; -;
MGD: MGI:2181676; CCR1L.
DR GO:GO:0016021; C:Integral to membrane, IEA.
DR GO:GO:0016493; F:C-C chemokine receptor activity, IEA.
DR GO:GO:0004872; F:receptor activity, IEA.
DR GO:GO:0001584; F:rhodopsin-like receptor activity, IEA.
DR GO:GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR InterPro: IPR005183; CC_11_receptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.

Query Match 87.7%; Score 1596; DB 11; Length 350;
 Best Local Similarity 85.4%; Pred. No. 9.2e-11;
 Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

Query 1 MLEBONOSTDYEEENENNGTYDSQYELICIKEDVREFAKVLPEFLTVFTVIGLAGNS 60
 DB 1 MALEINQSAEYEEENENNGTYDSQYEVICIKKEVRQFAKVLPEFLTVFTVIGLAGNS 60
 QY 1 MVAIYAYKKORTDYIINLAVADLLFTLPFMAVNAVHGVNLKIMKIKTSALYT 120
 DB 61 VVAIYAYKKORTDYIINLAVADLLFTLPFMAVNAVHGVNLKIMKIKTSALYT 120
 QY 121 LNFVSGMQLACISIDRYVAATKVPDSQGVKPCWIIICFCVMAAILLSIPQVFTVND 180
 DB 121 VNFVSGMQLACISIDRYVAATKVPDSQGVKPCWIIICCCVMAAILLSIPQVFTVND 180
 QY 121 NARCFIPFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISPLK 240
 DB 181 NARCFIPFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISPLK 240
 QY 241 VLLTVIVFIYVITQLPYNIYKFCRAIDIIYSLITSCNMRMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVIVFIYVITQLPYNIYKFCRAIDIIYSLITSCNMRMDIAIQVTSIALFHSCLNP 300
 QY 301 ILVFMGASFKNYIMKAKKYGSWRRQOSVEEPFDEGPTPTSTSI 350
 DB 301 ILVFMGASFKNYIMKAKKYGSWRRQOSVEEPFDEGPTPTSTSI 350

RESULT 2

08QCM1 PRELIMINARY; PRT; 350 AA.

AC 08QCM1; TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Chemokine receptor CCR11 homolog.
 GN CCR11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK030643; BAC27061.1; -
 DR MGD; MGI:2181676; Ccr11.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; IEA.
 DR InterPro; IPR005383; CC 11 receptor.
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PRO1558; CHEMOKINER11.
 DR PRINTS; PRO0237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEPT_F1_2; 1.
 SQ SEQUENCE 350 AA; 39562 MW; DAACD9D798E5A13 CRC64;

Query Match 87.6%; Score 1594; DB 11; Length 350;
 Best Local Similarity 85.4%; Pred. No. 1.4e-130;
 Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

Query 1 MLEBONOSTDYEEENENNGTYDSQYELICIKEDVREFAKVLPEFLTVFTVIGLAGNS 60
 DB 1 MALEINQSAEYEEENENNGTYDSQYEVICIKKEVRQFAKVLPEFLTVFTVIGLAGNS 60
 QY 1 MVAIYAYKKORTDYIINLAVADLLFTLPFMAVNAVHGVNLKIMKIKTSALYT 120
 DB 61 VVAIYAYKKORTDYIINLAVADLLFTLPFMAVNAVHGVNLKIMKIKTSALYT 120
 QY 121 LNFVSGMQLACISIDRYVAATKVPDSQGVKPCWIIICFCVMAAILLSIPQVFTVND 180
 DB 121 VNFVSGMQLACISIDRYVAATKVPDSQGVKPCWIIICCCVMAAILLSIPQVFTVND 180
 QY 121 NARCFIPFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISPLK 240
 DB 181 NARCFIPFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISPLK 240
 QY 241 VLLTVIVFIYVITQLPYNIYKFCRAIDIIYSLITSCNMRMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVIVFIYVITQLPYNIYKFCRAIDIIYSLITSCNMRMDIAIQVTSIALFHSCLNP 300
 QY 301 ILVFMGASFKNYIMKAKKYGSWRRQOSVEEPFDEGPTPTSTSI 350
 DB 301 ILVFMGASFKNYIMKAKKYGSWRRQOSVEEPFDEGPTPTSTSI 350

RESULT 3

08QCM9 PRELIMINARY; PRT; 350 AA.

AC 08QCM9; TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Chemokine receptor CXCR.
 GN CXCR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ.
 RA Tomason J.R., Nibbs R.J.;
 RT "Characterization of mouse CXCR, a receptor for the lymphocyte-
 RT attracting chemokines TBCK (CCL25), SLK (CCL21) and MIP-3beta (CCL19):
 RT comparison to human CXCR."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072796; AAL68400.1; -
 DR MGD; MGI:2181676; Ccr11.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; IEA.
 DR InterPro; IPR005383; CC 11 receptor.
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PRO1558; CHEMOKINER11.
 DR PRINTS; PRO0237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEPT_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 350 AA; 39544 MW; D017CC29749C8C5 CRC64;

Query Match 87.6%; Score 1593; DB 11; Length 350;
 Best Local Similarity 85.1%; Pred. No. 1.7e-130;
 Matches 298; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

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QY 1 MLEQKOSTDYEEENKNGTDYSGOYELICIKEDVEBAKVELPVLITVIVIGLAGNS 60
DB 1 MLELNQSGHEYYEENENMYTHDYSQYETICKEKVEKPAKFLAFVAFVIGLAGNS 60
QY 61 MVAIYAYKQRTKTDVYIINLAVADLLFLTPPMVAVNAGVGLKIMCKITSALYT 120
DB 61 VVAIYAYKQRTKTDVYIINLAVADLLFLTPPMVAVNAGVGLKIMCKITSALYT 120
QY 121 LNFVSGMOPLACISIDRYAVATKVPSSQSGVKPCMIICGVMAAILLSIPOLVYTYND 180
DB 121 VNFVSGMOPLACISIDRYAITKABSSQSGAGPCMIICGVMAAILLSIPOLVYTYNQ 180
QY 181 NARCIPIPRVYIGTSMKALIOMLEICIGFVPEFLMGVCYFITATLMKMPNIXISPLK 240
DB 181 NARCTPIFPHHLGTSIKASIQMLEIGIGFVPEFLMGVCYASTARALIKMPNIXKSRPLK 240
QY 241 VLLTVIVIVITQLPYNIYKFCRAIDIIYSLTSCNMSKRMIDIAQVETALFHSCLNP 300
DB 241 VLLAVVAVVITQLPYNIYKFCQALDAILYLLTSCNMSKRMIDIAQVETALFHSCLNP 300
QY 301 ILYVFMGASFKNYVMKAKKYSWRQSQVEEPFDESEPTSTPSI 350
DB 301 ILYVFMGASFKNYVMKAKKYSWRQSQVEEPFDESEPTSTPSI 350

RESULT 4
Q9ESK1 PRELIMINARY; PRT; 221 AA.
AC Q9ESK1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative G-protein coupled receptor GPCR14 (Fragment).
GN GPCR14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Harlan Sprague-Dawley;
RC Carroll S.L., Miller M.J., Benedict-Hamilton H.M.;
RT "Identification and characterization of novel G-protein coupled
RT receptors expressed in regenerating peripheral nerve.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DB EMBL; AF090348; AAC24470.1; -
DB GO; GO:0016021; C:Integral to membrane; IEA.
DB GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DB GO; GO:0004872; F:receptor activity; IEA.
DB GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DB GO; GO:0007186; P:G-protein coupled receptor protein signaling. .; IEA.
DB InterPro; IPR005382; CC 10 receptor.
DB InterPro; IPR002276; GPCR_Rhodopsn.
DB Pfam; PF00001; 7tm_1; 1.
DB PRINTS; PRO1557; CHEMOKINER10.
DB PROSITE; PRO0237; GPCR_HODOPSN.
DB PROSITE; PS00262; G_PROTEIN_RECPT_F1_1; 1.
DB PROSITE; PS00262; G_PROTEIN_RECPT_F1_2; 1.
DB KEGG; K00001; GPCR.
FT NON_TER 1 1
FT NON_TER 221 221
SQ SEQUENCE 221 AA; 24342 MW; 5622DD6073738A6C CRC64;

Query Match
Best local similarity 50.1%; Score 912; DB 11; Length 221;
Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 96 FMAVNAVHGVTJCKINCKITSAIYLTNYSQMOFLACISIDRYAVATKVPSSQSGVKPCW 155
DB 19 FMAVNAVHGVTJCKINCKITSAIYLTNYSQMOFLACISIDRYAVATKVPSSQSGVKPCW 78

QY 156 IIFGVMAAILLSIPOLVYTYNDNARCIPIPRVYIGTSMKALIOMLEICIGFVPEFLI 215

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DB 79 IICCVTAAILLSIPOLVYTYNENARCTPVPFPHLGTSLKASIQMLEIFIGFVPEFLI 138
QY 216 MGVCYFITATLMKMPNIXISPLKALITVYIYFITQLPYNIYKFCRAIDIIYSLTSC 275
DB 139 MGVCYFITATLMKMPNIXISPLKALITVYIYFITQLPYNIYKFCRAIDIIYSLTSC 198
QY 276 NMSKRMIDIAQVETALFHSCL 298
DB 199 NMSKRMIDIAQVETALFHSCL 221

RESULT 5
Q8H2R6 PRELIMINARY; PRT; 378 AA.
AC Q8H2R6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CC chemokine receptor 7.
GN CCR7.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22471764; PubMed=12406887;
RA Choi Y.K., Fallert B.A., Murhey-Corb M.A., Reinhart T.A.;
RT "Simian immunodeficiency virus dramatically alters expression of
RT homeostatic chemokines and dendritic cell markers during infection in
RT vivo".
RL Blood 101:1684-1691 (2003).
DR EMBL; AF508731; AAN47099.2; -
KW Receptor.
SQ SEQUENCE 378 AA; 42876 MW; D031BB48B29F08EF CRC64;

Query Match
Best local similarity 36.1%; Score 657; DB 6; Length 378;
Matches 143; Conservative 65; Mismatches 122; Indels 38; Gaps 7;

QY 5 QNOSTDYEEENKNGTDYSGOYELICIKEDVEBAKVELPVLITVIVIGLAGNSMVA 64
DB 25 QNOSTDYEEENKNGTDYSGOYELICIKEDVEBAKVELPVLITVIVIGLAGNSMVA 81
QY 65 IYAYKQRTKTDVYIINLAVADLLFLTPPMVAVNAGVGLKIMCKITSALYTINFEV 124
DB 82 IYAYKQRTKTDVYIINLAVADLLFLTPPMVAVNAGVGLKIMCKITSALYTINFEV 141
QY 125 SGMFLACISIDRYAVATKVPSSQSGVKPCMIICGVMAAILLSIPOLVYTYND 180
DB 142 SGMFLACISIDRYAVATKVPSSQSGVKPCMIICGVMAAILLSIPOLVYTYND 201
QY 181 NA-----RCIPIPRVYIGTSMKALIOMLEICIGFVPEFLMGVCYFITATLMKMPNIXI 235
DB 202 SSSSQMARCCLITEH---VEAFTTQVAGVIGFVPEFLMGVCYFITATLMKMPNIXI 258
QY 236 SRPLKVLTVIVITQLPYNIYKFCRAIDIIYSLTSCNMSKRMIDIAQVETALFHSCL 295
DB 259 NKAIVIAVAVVITQLPYNIYKFCRAIDIIYSLTSCNMSKRMIDIAQVETALFHSCL 318
QY 296 SCNPIIYVFMGASFKNYVMKAKKYSWRQSQVEEPFDESEPTSTPSI 350
DB 319 SCNPIIYVFMGASFKNYVMKAKKYSWRQSQVEEPFDESEPTSTPSI 369
QY 342 TEPSTPS 349
DB 370 AETTTTS 377

RESULT 6
Q8CASA2 PRELIMINARY; PRT; 378 AA.

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AC 08CAS2;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Chemokine.
GN CCR7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA THE FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK037965; BAC29909.1; -.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IMP.
DR GO; GO:0006935; P:chemotaxis; IMP.
DR GO; GO:0006955; P:immune response; IMP.
DR InterPro; IPR001064; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1_2; 1.
SQ SEQUENCE 378 AA; 42855 MW; F027451989B59683 CRC64;

Query Match 35.6%; Score 648; DB 11; Length 378;
Best Local Similarity 38.6%; Pred. No. 3e-48;
Matches 140; Conservative 67; Mismatches 128; Indels 28; Gaps 7;

QY 5 QNOSTDYIYENMNGTYDSQYELICIEDVREPKVLPVPLTVFVIGLAGNSMYA 64
DB QDVTDDYIGENT--TVDTLVESVCFKDDVTFPAMFLPVWYSIICFVGLGNGVL 81
QY 65 IYAYVKQRTKTDVYIINLAVADLLFLFPVAVAVAGVGLKIMCKITSALYTLNFV 124
DB 82 TYIFPRKIKMTDYLINLAVADILFLFLFPVAYSAKSWIFGVYLCIGIGIKLSF 141
QY 125 SGMQFLACISIDRYAVATKVP--QSGVGFCEWIIICCVMAAILLSIPOLVFTYND 180
DB 142 SGMILLLCISIDRYVAIVQAVSHRRARVLLISKSCVGIWMLALFLSIPELLYSGLOK 201
QY 181 NA-----RCIPPRVILGSMKAL--IQMLEICIGVVPFLINGVCYFTARTLMKMPRI 233
DB 202 NSEEDILRC-----SLVSAQVEALITIQVAGWFGVLPMANSPCYLITITLQARNF 256
QY 234 KIRPLKVLITVIVITVQLPYNIVKFCRAIDITSLTSCNMGKMDIAIQVETSLAL 293
DB 257 ERNKAIKVILIAVVVIVFQLPYNGVLAQTVANFNITSSCETSKOLIAVDVYISLAS 316
QY 294 FHSCLNPILVPMGASPKVVMCAKYGKSWROR-----QSVPEPFDEGPTSPS 346
DB 317 VRCCVVPFLYAFIGVFRSDLPKLPDGLGLOSERLRHWSSCRHANASVNE--AETTT 374
QY 347 TFS 349
DB 375 TFS 377

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DE Chemokine receptor 7.
GN CCR7.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9923;
RN [1]
RP SEQUENCE FROM N.A.
RC Shinkai H., Muneta Y., Awata T., Uenishi H.;
RT "Molecular cloning and mapping of swine chemokine receptor 7 (CCR7).";
RT Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB090356; BAC57561.1; -.
DR EMBL; AB090872; BAC57929.1; -.
DR EMBL; AB090870; BAC57929.1; JOINED.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0077186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR001064; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1_2; 1.
SQ SEQUENCE 380 AA; 42851 MW; 948B2794C6A76AD8 CRC64;

Query Match 35.5%; Score 645.5; DB 6; Length 380;
Best Local Similarity 37.3%; Pred. No. 4.9e-48;
Matches 140; Conservative 73; Mismatches 119; Indels 43; Gaps 9;

QY 1 MALDQNSTDYIYENMNGTYDSQYELICIEDVREPKVLPVPLTVFVIGLAGNS 60
DB 22 VCLQDVTDDYIGDNT--TVDTLVESVCFKDDVTFPAMFLPVWYSIICFVGLGNG 78
QY 61 MVAIYAYVKQRTKTDVYIINLAVADLLFLFPVAVAVAGVGLKIMCKITSALYTLNFV 120
DB 79 LVMLTYIFPRKIKMTDYLINLAVADILFLFLFPVAYSAKSWIFGVYLCIGIGIKLSF 138
QY 121 LNPVSGMFLACISIDRYAVATKVP--QSGVGFCEWIIICCVMAAILLSIPOLVFTY 176
DB 139 ISFSGMILLLCISIDRYVAIVQAVSHRRARVLLISKSCVGIWMLALFLSIPELLYSGLOK 198
QY 177 TVDNNA-----RCIPPRVILGSMKAL--IQMLEICIGVVPFLINGVCYFTARTLMKMPRI 229
DB 199 GTQSSSEQALRC-----SLITEHVEALITIQVAGWFGVLPMANSPCYLITITLQARNF 253
QY 230 MPNIKIRPLKVLITVIVITVQLPYNIVKFCRAIDITSLTSCNMGKMDIAIQVETSLAL 288
DB 254 ARNERBKAIKVIILIAVVVIVFQLPYNGVLAQTVANFNITSGTSCETSKOLIAVDVYISLAS 313
QY 289 ESTLPHSCNPILVPMGASPKVVMCAKYGKSWROR-----QSVPEPFDEGPTSPS 346
DB 314 YSLACVRCVVPFLYAFIGVFRSDLPKLPDGLGLOSERLRHWSSCRHANASVNE--AETTT 374
QY 375 TFS 377

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01-MAY-2000 (Tremblrel. 13, last sequence update)
 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Chemokine receptor CCR9 (CC chemokine receptor 9A).
 GN CCR9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99248139; PubMed=10229797;
 RX Zabolos A., Gutierrez J., Varona R., Ardavin C., Marquez G.,
 RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
 receptor for the chemokine TECK."
 RL J. Immunol. 162:5671-5675 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yu C.-R., Peden K.W.C., Farber J.M.,
 RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
 15)."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ132337; CAB43477.1; -
 DR EMBL; AF145439; AAF66699.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR004069; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1531; CHEMOKINER9.
 DR PROSITE; PS00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_1; 1.
 DR Receptor.
 SQ SEQUENCE 369 AA; 42015 MW; F27CEACFB6844C CRC64;
 Query Match 35.3%; Score 643; DB 4; Length 369;
 Best Local Similarity 36.4%; Pred. No. 7,9e-48;
 Matches 120; Conservative 75; Mismatches 117; Indels 18; Gaps 4;
 QY 6 NOSTDYEE-NEMNGTYDSQYELICIKEDYREPAKVLPEFLTVFVIGLAGSMVA 64
 DB 12 NMADVGSSTSMEDYVNFNFTDFCEKNVQFASHFLPELVLFVIGLAGSLVIL 71
 QY 65 IYAYKQRTKTDVYLINAVADLLFLPFMAVNAHGVLGKIMKITSALTALFV 124
 DB 72 VYVYCTRVKTMIDMFLNLAIADLLFLPFWALAAADQMKQTFMCKVNSMTKMFY 131
 QY 125 SGWQFLACISIDRYVAVTKVPSQSGVGRPCW-----IICFVMAAILLSIPOLVF 175
 DB 132 SCVLLMNCISVDYKIAIQ-----AMRAHTRKREKLLYSKMCFTIIVAAALCPEILY 186
 QY 176 YTVNDN--ARCIPIFRYIGTSMKALIQMLEICIGFVFPFLMGVCYITRTIMKFN 232
 DB 187 SQIKESGIAICTMYVPSDESTKLSAVLTKVILGFLPFVMAACCYIIIIHTLIQAKK 246
 QY 233 IKTSRLKXLLTVIVIVITQLPYINVKFCRAIDIIYSLTSCNMSKMDIAIQTESIA 292
 DB 247 SSKKALKKTIITVIVFVLSQFPYNCILVQITDAAMTISNCAVSTNIDICQVYOTIA 306
 QY 293 LFHSCINPILYVFGASFKNYVMKAKKYG 322
 DB 307 FFHSCINPVLVYFVGERFRDLVKTLKNG 336
 RESULT 9
 Q8CH33 PRELIMINARY; PRT; 369 AA.
 AC Q8CH33;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, last sequence update)

01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Chemokine receptor CCR9.
 GN CCR9.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=LEW; TISSUE=Thymus;
 RC Cugini D., Norris M., Remuzzi G.;
 RT "Rattus norvegicus chemokine receptor CCR9."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF458780; AAF76889.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR004069; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1531; CHEMOKINER9.
 DR PROSITE; PS00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_1; 1.
 DR Receptor.
 SQ SEQUENCE 369 AA; 41977 MW; 9935561D95FC52C CRC64;
 Query Match 35.3%; Score 643; DB 11; Length 369;
 Best Local Similarity 36.3%; Pred. No. 7,9e-48;
 Matches 119; Conservative 76; Mismatches 111; Indels 22; Gaps 5;
 QY 10 DYVYEEENMGTY---DYSQYELICIKEDYREPAKVLPEFLTVFVIGLAGSMVAIY 66
 DB 16 DYSIDSTASTDDYDYNLFSSP--FCKKNVQFASHFLPELVLFVIGLAGSLVILV 73
 QY 67 AYKQRTKTDVYLINAVADLLFLPFMAVNAHGVLGKIMKITSALTALFV 126
 DB 74 WYCTRVKTMIDMFLNLAIADLLFLPFWALAAQWQFQFMCKVNSMTKMFYSC 133
 QY 127 WQFLACISIDRYVAVTKVPSQSGVGRPCW-----IICFVMAAILLSIPOLVF 177
 DB 134 VLLMNCISVDYKIAIQ-----AKAQWRKRLYSKMCFTIIVAAALCPEILY 186
 QY 178 VNND---ARCIPIFRYIGTSMKALIQMLEICIGFVFPFLMGVCYITRTIMKFN 234
 DB 189 ISGSGIAICTMYVPSDESTKLSAVLTKVILGFLPFWMAFCYIIIIHTLIQAKKS 248
 QY 235 ISRLKXLLTVIVIVITQLPYINVKFCRAIDIIYSLTSCNMSKMDIAIQTESIALF 294
 DB 249 KHKALKKTIITVIVFVLSQFPYNCILVQAVDAVTMFTISNCTSTNIDICQVYOTIA 308
 QY 295 HSCINPILYVFGASFKNYVMKAKKYG 322
 DB 309 HSCINPVLVYFVGERFRDLVKTLKNG 336
 RESULT 10
 Q8RIVO PRELIMINARY; PRT; 367 AA.
 AC Q8RIVO;
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE CC chemokine IARC specific receptor.
 GN CCR6 OR CCR6B OR MCCR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Tanaka Y.;
 RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
 for CC Chemokine LARC."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB016031; BAA82443.1; -
 DR MGD; MGI:1333797; Ccr6.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR004067; CC_6_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1529; CHEMOKINER6.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6D3 CRC64;
 Query Match 33.6%; Score 611; DB 11; Length 367;
 Best Local Similarity 38.2%; Pred. No. 4,8e-45;
 Matches 130; Conservative 60; Mismatches 124; Indels 26; Gaps 8;
 QY 8 STDYVEENENNGYDSQYELI-----CIKEDVREFAKVELFVFLITVFGVGLAGNSM 61
 DB 3 STESYFGTDD---YDNTVEYSIPDPGSCLEVEVNFVKVFIAYSLICVGLGNIM 58
 QY 62 VVAIYAYKQKRTKTDVYILNLAVADLLFLTFPMNAV-NAHGVMVGKIMCKITSLALT 120
 DB 59 VVMTFAPFKKRSMTDVLNLMAITDILFVTLDFPMVTHATNIVPSDACLKMKGTVA 118
 QY 121 LNFVSGMFLACISIDRYVAATKVPSSGSGVKPCW---IICFVMAAILLSIPQLVF- 175
 DB 119 VNENGMGLLACISMDRYIAIVQATKSPRVSRRLTSHSKVICAVWFSLIISSPTEIFN 178
 QY 176 --YVNDNARCIPIFPRLIGTS---MALLQMEICIGFVFPFLINGVCYFTARTLMK 229
 DB 179 KKEYLQDQDVC--EPRRYSVSEPTWELGLGLEFFGFTPLLFVFCYLFITKLVLQ 235
 QY 230 MPNIKSRPLKLVIVFIVTQLEFYNIVKFCRAIDIIYSLTSCMSKMDIAIOVTE 289
 DB 236 AONSGRHAIIVLAVAVLFLACQIPHNMLLVLRVN-TGVNARSCTEKLAVATRVAAE 294
 QY 290 SIALFHSCLNPLIYFENGASFKYVMKAKYSGWRQRQ 329
 DB 295 VLAFLHSCINPLVLAFLIQKFRNYFMKIMKDVCMCRNRKX 334
 RESULT 11
 ID 042444 PRELIMINARY; PRT; 368 AA.
 AC 042444;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Chemokine receptor
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OC NCBI_TaxID=8022;
 RX MEDLINE=99260342; PubMed=10331499;
 RA Daniels G.D., Zou J., Charlemagne J., Partula S., Cunningham C.,
 RA Secombes C.J.;
 RT "Cloning of two chemokine receptor homologs (CXC-R4 and CC-R7) in
 RT rainbow trout Oncorhynchus mykiss."
 RL J. Leukoc. Biol. 65:684-690 (1999).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ003159; CA05917.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 368 AA; 41523 MW; 3B28E2D4C47B821A CRC64;
 Query Match 32.2%; Score 586.5; DB 13; Length 368;
 Best Local Similarity 37.3%; Pred. No. 6,5e-43;
 Matches 120; Conservative 58; Mismatches 125; Indels 19; Gaps 4;
 QY 22 YVYSQY-----ELICIKEDVREFAKVELFVFLITVFGVGLAGNSVMVAIYAYK 70
 DB 17 YDYDSSFFPTGDEDVDNPMCKSAVRARFGQYEBPLWYSVILGSLNLVVMYIYHFR 76
 QY 71 KO-RKTDVYIILNLAVADLLFLTFPMNAVNAHGMVVGKIMCKITSLALTNLNFSNQF 129
 DB 77 QRLKMTMDIYILNLAVADLFLGTLPLWAVEANQMSFGLGCKVTSAFYKINFFSSML 136
 QY 130 LACISIDRYVAATKVPSSGSGVKP---CWIIICFVMAAILLSIPQLVFYVND---NA 182
 DB 137 LNCISIDRYVAATKVPSSGSGVKPRLSCSKFVCAVWLLAVLALPEFMFANVXELDQF 196
 QY 183 RCIPIFPRLIGTSKALIQMLEICIGFVFPFLINGVCYFTARTLMKPNIKSRPLKVL 242
 DB 197 YCTMYWYSNQNRRTKIVIVGLQICMGFCLPLVWFCVAGIIRILTKRSPQKHALAVI 256
 QY 243 LVVIVFIVTQLEFYNIVKFCRAIDIIYSLTSCMSKMDIAIOVTEIALFHSCLNPL 302
 DB 257 LVVAVFVLSQLEPVNSVVMETQANSTQTDCAAKRNVSYQLKSLAYTHACLNPL 316
 QY 303 YVFMGASFKNYVMKAKYSGWSN 324
 DB 317 YVFGVRFRRDILKLRITVHCW 338
 RESULT 12
 ID 08HZ87 PRELIMINARY; PRT; 374 AA.
 AC 08HZ87;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE CC chemokine receptor 6.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Choi Y.K., Fallert B.A., Murphy-Corb M.A., Reinhart T.A.;
 RT "Simian Immunodeficiency Virus Dramatically Alters Expression of
 RT Homeostatic Chemokines and Dendritic Cell Markers During Infection In
 RT Vivo."
 RL Blood 0:0-0 (2002)
 DR EMBL; AF508730; AAN47098.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR004067; CC_6_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1529; CHEMOKINER6.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 374 AA; 42649 MW; A64A515BAC09E928 CRC64;

Query Match	32.1%	Score 583	DB 6	Length 374
Best Local Similarity	35.2%	Pred. No. 1.3e-43		
Matches 119	Conservative 73	Mismatches 114	Indels 32	Gaps 8

Query	8	STDIYYEENANGTYDSQYELICIKEDVREFAKPLPVFLTFVYIGLAGNSMVAIYA	67
Db	23	NTSYVADSEM-----LLCTLHEVROFSRLFPVIAVSLICVGLIGNLIVITPA	72
Qy	68	YRKQKRTKDYVITLNLAAVDLLFTLPEFMAV-NAVHGWLGLKMKITSLATLTNPFVG	126
Db	73	FKKARSMIDVYLLKMLADILFVTLPEFAVSAITGAMPFSNACKLKGITAINFNG	132
Qy	127	WQFLACISIDRYAVATKVPQSGV-----GKPCWITGCVMAAILISIPOLV--Y	176
Db	133	MLLTITISIDRYAIAIVQATKSFRLRYFTLLRSK--VICLIWVGSGVLSSTFIENCK	189
Qy	177	TVNDNARCIPIEPYLAGTS---MVALQMEICIGVVFLLMGVCYFTATLTKMN	232
Db	190	NIGGSVC--EPKQIYVSEPKKMLMLGELFGFFILPMVIMFYVYVTLVQAON	246
Qy	233	IKISRELKXLLTVIVFIVTOLPVNIYKFCDAIDILYSITSCMSKRDIALQVETSA	292
Db	247	SKRKRIKRIYAVVLFVLAQCPHNHMLVLTAAAN-LGNMRSCHSEKLGXTKTEVLA	305
Qy	293	LPHSCINPLIYFMGASPNYIMKAKIKYGSWRRQRS	330
Db	306	FLHCCLNPVLYAFIQGFENYFLKTMKQMCVRRKYS	343

RESULT 13	Q9N0Z0	PRELIMINARY:	PRT:	343 AA.
AC	Q9N0Z0:			
DT	01-OCT-2000 (TRENBLrel. 15, Created)			
DT	01-OCT-2000 (TRENBLrel. 15, Last sequence update)			
DT	01-JUN-2003 (TRENBLrel. 24, Last annotation update)			
DE	Str133.			
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey) .			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC	Cercopitheidae; Cercopithecus.			
OX	NCBI_taxid=9531;			
OX	NCBI_taxid=9531;			
RA	SEQUENCE FROM N.A.			
RA	MEDLINE=40261727; PubMed=10795681;			
RA	Pohlman S., Lee B., Meister S., Krumdiegel M., Leslie G., Doms R.W.,			
RA	Kirchoff F.;			
RA	Submitted (FEb-2000) to the EMBL/Genbank/DBJ databases			
CC	-1- SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN (BY SIMILARITY) .			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL: AF237559; AAF68392.1; -			
DR	GO: GO:0016021; C: integral to membrane; IEA.			
DR	GO: GO:0004872; P: receptor activity; IEA.			
DR	GO: GO:0001584; P: rhodopsin-like receptor activity; IEA.			
DR	GO: GO:0007186; P: G-protein coupled receptor protein signaln. . .; IEA.			
DR	InterPro: IPR000276; GPCR_Kinopsn.			
DR	Pfam: PF00001; 7tm.1.1.			
DR	PRINTS: PR00237; GPCR_RHODOSP.			
DR	PROSITE: PS00237; G-PROTEIN REEP_F1.1; 1.			
DR	PROSITE: PS50262; G-PROTEIN REEP_F1.2; 1.			
KW	G-protein coupled receptor; Receptor; Transmembrane.			
SEQUENCE	343 AA; 39589 MW; A75B7A0751C13455 CRC64;			

Query Match	31.8%	Score 578	DB 6	Length 343
Best Local Similarity	33.7%	Pred. No. 3.3e-42		

	Matches	120;	Conservative	73;	Mismatches	131;	Indels	32;	Gaps	8
Oy	10	DYYEENEMNGTYY	SOVELLICTEDYREFRANKVLPFLRTIVETIGLAGNSMVAIYAY	69						
Db	5	DHYDDEFFESFENS	SQKE---HQDLQSBSKVPFCMYLVFPVCGLVNSLVITISFY	60						
Oy	70	KKORTKDVTYINLANVDLLFTLPFWAVAAVAGWVLGKIMCKITSALYLNAFVSQMCF		129						
Db	61	HKGOSLDVPLVNLPLADLVFVCTLLPFMAVAGIHWMFGQCMTLTIGVYINFTYSMLI		120						
Oy	130	LACISIDRYAVATKVPS--QGSGVKPCWK--IICCCVMMAILSLIPOLVFITY--NDNAR		183						
Db	121	LTCITVRFVVVATRAYNQQAQRMTWGKVICLIWIIVLSVLPDIYGNVFNLDKLI		180						
Oy	184	CIFPFPYLGSMALKOMLEICIGFVFPFLMGVCYFITARTMKPNIKSRPLKVL		243						
Db	181	C-----RYHDEISTVLATQMTLGFELPLLTMVYCYSVIKITLLHAGPGPKHSLSKIIF		235						
Oy	244	TTVIVFIVTQLPVNIYVFCRAIDIIYSLLTSCNNKSMDIAIQVESTIALFHSCANPLY		303						
Db	236	LVMAVFLITQPPEPFLVXLIRSTHEVEYAAMTSFHYT-----IYTEAIAYLRACINPVL		289						
Oy	304	VFMASAKNYMKYAKAXYG-----SMRRQSQSVBEPPSDEGPTEPSTESI		350						
Db	290	AFVSLKRKFQFWKIVKDIOGCLPYGVSHQMSSDNRK--TFSSAHNVATISMFL		343						
	RESULT 14									
	Q9EQJ6	PRELIMINARY;	PRT;	351 AA.						
AC	Q9EQJ6:									
DT	01-MAR-2001 (TREMBLrel. 16, Created)									
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)									
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)									
DE	Chemokine receptor CXCR6.									
GN	CXCR6.									
OS	Mus musculus (Mouse).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
NCBI_TaxID=10090;										
RN	[1]									
RN	SEQUENCE FROM N.A.									
RC	STRAIN=C57BL/6;									
RA	MEDLINE=21177382; Pubmed=11017100;									
RA	MacIoudian M., David A., Engel S., Ryan J.F., Cyeter J.G.;									
RT	"A transmembrane CXC chemokine is a ligand for HIV-coreceptor Benzo."									
RL	Nat. Immunol. 1:298-304 (2000).									
RN	[2]									
RN	SEQUENCE FROM N.A.									
RC	STRAIN=C57BL/6J; TISSUE=Heart;									
RA	MEDLINE=22354683; Pubmed=12466851;									
RA	The FANTOM Consortium,									
RT	"The Riken Genome Exploration Research Group Phase I & II Team;									
RL	"Analysis of the mouse transcriptome based on functional annotation of									
RL	60,770 full-length cDNAs.";									
DR	Nature 420:563-573(2002).									
DR	EMBL; AF301018; AAC34357.1; -									
DR	EMBL; AK052901; BAC35196.1; -									
DR	MGD; MGI:1934582; Cxcr6.									
GO	GO:0016494; F-C-X-C chemokine receptor activity; IDA.									
DR	InterPro; IPR000276; GPCR_Rhodopsn.									
DR	Pfam; PF00001; 7tm_1; 1.									
DR	PRINTS; PRO0237; GPCRHDOPSN.									
DR	PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.									
DR	PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.									
KM	Receptor.									
SQ	SEQUENCE 351 AA; 40468 MW; 5658788372B4C65A CRC64;									
	Query Match 31.1%; Score 566.5; DB 11; Length 351;									
	Best Local Similarity 35.4%; Pred.No.3.4e-41;									
	Matches 127; Conservative 70; Mismatches 125; Indels 37; Gaps 10;									
Oy	10 DYYEEN--EMNGYVDSQVELLICKEVVR--EFANKVLPFLRTIVETIGLAGNSMVAI									

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Db      12 DGHVEGDWLFNNSDSSQ-----ENKRFLEKRENFLEPCVYLVVFGLGSLVLI 64
QY      66 YAYVKKORTKDVYLLNLAVADLLFLPLPFMAVANAHVGLGKINCKITSALYTLNFS 125
Db      65 YIFVQKRTLDVFLNLPLADLVFVCTLPFMAVAGTEVFGVMCKTLRGMVTNMFY 124
QY      126 GMOFLACISIRYAV--TKVPSGSGVKPCW--IICPCVMAAILLSIPQVLFYVND 180
Db      125 SMLTLCITVRFLVAVQATGAFNQAQK--IMQVQICLLIIVVSLVSLPQIIYGHVQD 183
QY      181 NARCIPIPRYLGTSKALLIQMLEICIGFVVPFLIMGVCFYITARTLMKMNKISRLPK 240
Db      184 IDKI---CQXHEISISTMVLVIQWTLGFFLPLLTMLICSGIITKLHANNPQKHSK 240
QY      241 VLLTVYVFIYQLPYNYVVKFCRAIDIIYSLITSGNSKRDIAIQTESIALFHSCLNP 300
Db      241 IIFLVVAVFLLQTFPFLNLAFLIQTSTWEYTTIS-----FKYALVTEALAYFRACINP 294
QY      301 ILVVMGASFKNYVMKAKKYG-----SWRRQSQVEEPFDSGPTSTPSI 350
Db      295 VLVAVFGKFRKNWKKMKDIGCLSHGVSSQWKSSEDSK--TCSASHNVEITSMFOL 351

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RESULT 15

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Q9BDS6 PRELIMINARY; PRT; 343 AA.
ID Q9BDS6
AC Q9BDS6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 24, last annotation update)
DE Orphan seven transmembrane receptor STRL33.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBT_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21134756; PubMed=1124524;
RA Wade-Evans A.M., Russell J., Jenkins A., Javan C.;
RT "Cloning and sequencing of cynomolgus macaque ccr3, gp15, and strl33:
RT potential coreceptors for HIV type 1, HIV type 2, and STV."
RT AIDS Res Hum Retroviruses 17:371-375(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF291671; AAK25742.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007166; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 343 AA; 39472 MW; 0961328F948E7784 CRC64;

```

Query Match 31.1%; Score 566; DB 6; Length 343;
 Best Local Similarity 33.1%; Pred. No. 3.7e-41;
 Matches 118; Conservative 73; Mismatches 133; Indels 32; Gaps 8;

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QY      10 DYVYEENMNGTYDYSQYELICIKEDVREFAKVFLEVFLLVFVIGLAGNSMVAATYAY 69
Db      5 DHYEDDGLNSPNDSSQEE---HODFLQFRKVFPCMYLVVFVCGLVGNSLVLTISIFY 60
QY      70 KKQRTKTDVYLLNLAVADLLFLPLPFMAVANAHVGLGKIMCKITSALYTLNFSGMQF 129
Db      61 HRLQSLTDLVFLNLPLADLVFVCTLPFWYAGIHFWIGQVMCKTLGVTYINFTSMLI 120
QY      130 LACISIDRYVAVTKVPS--QSGVGKPCW--IICPCVMAAILLSIPQVLFYV--NDNAR 183

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Db      121 LNCITVDRIIVVVKATKANQQAQKMTNGKVICLLINVISLVSIPQIIYGVNVDKI 180
QY      184 CIPIPRYLGTSKALLIQMLEICIGFVVPFLIMGVCFYITARTLMKMNKISRLPKVL 243
Db      181 C-----GYHDEISITVVLATQWTLGFFLPFLAMICYGVIIKTLHAGGFQGRRLKII 235
QY      244 TVYIVFIYQLPYNYVVKFCRAIDIIYSLITSGNSKRDIAIQTESIALFHSCLNPILY 303
Db      236 LVNAVFLTLQTFPFLNKLIRSTRMEYVANTSPHYT-----IYTEALAYFRACINPVL 289
QY      304 VVMGASFKNYVMKAKKYG-----SWRRQSQVEEPFDSGPTSTPSI 350
Db      290 AFVSLKFRKNFWKLVYDIGCLPYLGVSQWKSSEDSK--TFSASHNVEATSMFOL 343

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Search completed: April 13, 2004, 13:16:21
 Job time : 47 secs